

FIGURE 1

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCTCCGCGGGATCCTCTAGAGATCCCT
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA
CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGC
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGGAGGCACAGGTGGCCCCCACCACCCGGAGG
AGCAGCTCCTGCCCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGA
AGGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCT
TCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCCGGCCGTTAGGGTGTGTGCT
GTCCCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTCTGTCAGCGTGTGTACCAGCCCTTCC
TCACCACCTGCGACGGGCACCGGGCCTGCAGCACCTACCGAACCATTTATAGGACCGCCTAC
CGCCGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTACGCGTGTGTGCCCCGGCTGGAAGAG
GACCAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAG
GGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAG
TCAGATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCATCAACACCGC
CGGCAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTG
TGCCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAG
GAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCT
GGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCC
TCCTGGTGCACCTCCTTCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTC
CTGGAGGAGCAGCTGGGGTCTGCTCCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGG
CTGGACTGAGCCCCCTACGCGGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGGTC
CAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTTTTCTCCTC
CCCTTCCTCGGGAGGGTCCCCAGACCCTGGCATGGGATGGGCTGGGATTTTTTTTGTGAAT
CCACCCCTGGCTACCCCCACCCTGGTTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCA
GCTGAGGGAAGGTACGAGTTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCC
CGGAGGCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACATAAAAAATGAAA
CGTGAAGGGCGGCCGCGACTCT
AGAGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGT
TACAAAT

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FIGURE 2

MTDSPPPGHPEEKATPPGGTGHEGLSGGAADVASGVGSGRHRARLPARPLGCVLSRAHGDPV
SESFVQRVYQPFLTTCDGHRACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGAC
GAAICQPPCRNGGSCVQPGRRCRCPAGWRGDTQCSDVDECSARRGGCPQRCINTAGSYWCQCW
EGHSLSADGTL CVPKGGPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLAS
QALEHGLPDPGSLLVHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 93-97, 270-274

N-myristoylation sites.

amino acids 19-25, 78-84, 97-103, 100-106, 103-109, 157-163,
191-197, 265-271

Amidation site.

amino acids 26-30

Aspartic acid and asparagine hydroxylation site.

amino acids 152-164

Cell attachment sequence.

amino acids 130-133

EGF-like domain cysteine pattern signature.

amino acids 123-135

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T05T0T 8T8660

FIGURE 3

CGCTCGCCCCGTCGCCCCCTCGCCTCCCCGCAGAGTCCCCTCGCGGCAGCAGATGTGTGTGGG
 GTCAGCCCACGGCGGGGACTATGGTGAAATTCCCGGCGCTCACGCACTACTGGCCCCCTGATC
 CGGTTCTTGGTGCCCCCTGGGCATACCAACATAGCCATCGACTTCGGGGAGCAGGCCTTGAA
 CCGGGGCATTGCTGCTGTCAAGGAGGATGCAGTCGAGATGCTGGCCAGCTACGGGCTGGCGT
 ACTCCCTCATGAAGTTCTTACGGGTCCCATGAGTGACTTCAAAAATGTGGGCCTGGTGT
 GTGAACAGCAAGAGAGACAGGACCAAAGCCGTCTGTGTATGGTGGTGGCAGGGGCCATCGC
 TGCCGTCTTTCACACACTGATAGCTTATAGTGATTTAGGATACTACATTATCAATAAACTGC
 ACCATGTGGACGAGTCGGTGGGGAGCAAGACGAGAAGGGCCTTCCTGTACCTCGCCGCCTTT
 CCTTTCATGGACGCAATGGCATGGACCCATGCTGGCATTCTCTTAAAACACAAATACAGTTT
 CCTGGTGGGATGTGCCTCAATCTCAGATGTCATAGCTCAGGTTGTTTTTGTAGCCATTTTGC
 TTCACAGTCACCTGGAATGCCGGGAGCCCCCTGCTCATCCCGATCCTCTCCTTGTACATGGGC
 GCACTTGTGCGCTGCACCACCCTGTGCCTGGGCTACTACAAGAACATTACAGCATCATCCC
 TGACAGAAGTGGCCCCGAGCTGGGGGGAGATGCAACAATAAGAAAGATGCTGAGCTTCTGGT
 GGCCTTTGGCTCTAATTCTGGCCACACAGAGAATCAGTCGGCCTATTGTCAACCTCTTTGTT
 TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA
 CCCTGTGGGTACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCCTGCTTTTCG
 ACAAGAATAAACCCAGCAACAACTGGTGAGCACGAGCAACACAGTCACGGCAGCCACATC
 AAGAAGTTCACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTCGTGATGTTTTGGAC
 ACCCAACGTGTCTGAGAAAATCTTGATAGACATCATCGGAGTGGACTTTGCCTTTGCAGAAC
 TCTGTGTTGTTTCTTTGCGGATCTTCTCCTTCTTCCAGTTCAGTCACAGTGAGGGCGCAT
 CTCACCGGGTGGCTGATGACACTGAAGAAAACCTTCGTCTTGGCCCCAGCTCTGTGCTGCG
 GATCATCGTCTCATCGCCAGCCTCGTGGTCTACCTACCTGGGGGTGCACGGTGCAGCCC
 TGGGCGTGGGCTCCCTCCTGGCGGGCTTTGTGGGAGAATCCACCATGGTGCCTATCGCTGCG
 TGCTATGTCTACCGGAAGCAGAAAAAGAAGATGGAGAATGAGTCGGCCACGGAGGGGGAAGA
 CTCTGCCATGACAGACATGCCTCCGACAGAGGAGGTGACAGACATCGTGGAATGAGAGAGG
 AGAATGAATTAAGGCACGGGACGCCATGGGCACTGCAGGGACGGTCAGTCAGGATGACACTTC
 GGCATCATCTCTTCCCTCTCCCATCGTATTTTGTTCCTTTTTTTTGTGTTTTGTTTGGTAAT
 GAAAGAGGCCTTGATTTAAAGGTTTCGTGTCAATTCTCTAGCATACTGGGTATGCTCACACT
 GACGGGGGGACCTAGTGAATGGTCTTTACTGTTGCTATGTAAAAACAAACGAAACAACTGAC
 TTCATACCCCTGCCTCACGAAAACCCAAAAGACACAGCTGCCTCACGGTTGACGTTGTGTCC
 TCCTCCCCTGGACAATCTCCTCTTGGAACCAAAGGACTGCAGCTGTGCCATCGCGCCTCGGT
 CACCCTGCACAGCAGGCCACAGACTCTCCTGTCCCCCTTCATCGCTCTTAAGAATCAACAGG
 TTAAAACTCGGCTTCTTTGATTGCTTCCCAGTCACATGGCCGTACAAAGAGATGGAGCCC
 CGGTGGCCTCTTAAATTTCCCTTCTGCCACGGAGTTCGAAACCATCTACTCCACACATGCAG
 GAGGCGGGTGGCACGCTGCAGCCCGGAGTCCCCGTTCACTGAGGAACGGAGACCTGTGAC
 CACAGCAGGCTGACAGATGGACAGAATCTCCCGTAGAAAGGTTTGGTTTGAAATGCCCGGG
 GGCAGCAAACTGACATGGTTGAATGATAGCATTTCACCTCTGCGTTCTCCTAGATCTGAGCAA
 GCTGTCAGTTCTCACCCCCACCGTGTATATACATGAGCTAACTTTTTTAAATTGTCACAAAA
 GCGCATCTCCAGATTCCAGACCCTGCCGCATGACTTTTCTGAAGGCTTGCTTTTCCCTCGC
 CTTTCTCTGAAGGTCGCATTAGAGCGAGTCACATGGAGCATCCTAACTTTGCATTTTAGTTTT
 TACAGTGAAGTGAAGCTTTAAGTCTCATCCAGCATTCTAATGCCAGGTTGCTGTAGGGTAAC
 TTTTGAAGTAGATATATTACCTGGTCTGTCTATCCTTAGTCATACTCTGCGGTACAGGTAA
 TTGAGAATGTACTACGGTACTTCCCTCCCACACCATAACGATAAAGCAAGACATTTTATAACG
 ATACCAGAGTCACTATGTGGTCTCCCTGAAATAACGCATTTCGAAATCCATGCAGTGCAGTA
 TATTTTTCTAAGTTTTTGAAAGCAGGTTTTTTTCTTTTAAAAAATTATAGACACGGTTCAC
 AAATTGATTTAGTCAGAATTCCTAGACTGAAAGAACCTAAACAAAAAATATTTTAAAGATA
 TAAATATATGCTGTATATGTTATGTAATTTATTTTAGGCTATAATACATTTCTTATTTTCG
 ATTTTCAATAAAATGTCTCTAATACAAAAA

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FIGURE 4

MVKFPALTHYWPLIRFLVPLGITNIAIDFGEQALNRGIAAVKEDAVEMLASYGLAYSLMKFF
TGPMSTDFKNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYIINKLHHVDESV
GSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKYSFLVGCASISDVIAQVVFVAILLHSHLEC
REPLLIPILSLYMGALVRCTTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLALIL
ATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMPYGWLTEIRAVYPAFDKNNPSN
KLVSTSNVTAAHIKKFTFVCMAISLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLR
IFSFFPVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYLGVBHGATLGVGSL
AGFVGESTMVAIAACYVYRKQKKKMNESATEGEDSAMTDMPPTEEVTDIVEMRENE

Transmembrane domains:

amino acids 86-106, 163-179, 191-205, 237-253, 327-343, 357-374,
408-423, 431-445

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FIGURE 5

CCTGACAGAAGTGCCCCGGAGCTGGGGGAGATNCAACATTAAGAAGATGCTGAGCTTCTGGT
GCCNTTTGGCTCTAATTCTGGCCACACAGAGAANCAGTCGGCCTATTGTCAACCTCTTTGTT
TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA
CCCTGTGGGTCACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCCTGCTTTCG
ACAAGAATAACCCCAGCAACAACTGGTGAGCACGAGCAACACAGTCACGGCGGCCCCACATC
AAGAAGTTCACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTCGTGATGTTTTGGAC
ACCCAACGTGTCTGNGAAAATCTTGATAGACATCATCGGAGTGGACTTTGCCTTTGCAGAAC
TCTGTGTTGTTCTTTGCGGATCTTCTCCTTCTTCCCAGTTCAGTCACAGTGAGGGCGCAT
CTCACCGGGTGGCTGATGACACTGAAGAAAACCTTCGTC

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FIGURE 6

TGACGGAATCCCGGGCTGGGTATCCTGGTTTNGACAAGATAAACCCCCAGCAANAAATTGGG
GAGCAGGGCAAAACAGTNACGGGCAGCCCACATCAAGAAGTTCACCTTNGTTTGNATGGNTC
TGTCAACTCACGCTNTGTTTCGTGATGTTTTGGACACCCAAAGTGTTTGAGAAAATTTTGAT
AGACATNATCGGAGTGGANTTTGCCTTTGCAGAANTTTGNGNTGTTCCCTTTGCGGATTTTCT
CCTTTTTCCCAGTTCCAGTCACAGNGAGGGCGCATCTCACCGGGNGGNTGATGACANTGAAG
AAAACCTTTGTCCTTGCCCCCAGCTNTTTGGTGCGGATCATTGTCCTNATNGCCAGCCTTGT
GGTCCTACCCTACCTGGGGGTGCACGGTGCGACCCTGGGCGTGGGTTCCCTCCTGGCGGGCA

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FIGURE 7

TATTCCCAGTTCCGGTCACGGGGAGGGCGCATNTCACCGGGTGGCTGANGACACTGAAGAAA
ACCTTNGTCCTTGCCCCCAGNTTTGTGNTGCGGATNATCGTCCTCATCGCCAGCCTNGTGGT
CCTACCCTACCTGGGGGTGCACGGTGAGAC

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FIGURE 8

GCCCCGCGCCCGGCGCCGGGCGCCCGAAGCCGGGAGCCACCGCCATGGGGGCCTGCCTGGGA
GCCTGCTCCCTGCTCAGCTGCGCGTCCTGCCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAG
CTGCTGCCCCGCCAGCCGCAACTCCACCGTGAGCCGCCTCATCTTCAGTTCTTCCTCTTCC
TGGGGGTGCTGGTGTCCATCATTATGCTGAGCCCGGGCGTGAGAGTCTACAAGCTG
CCCTGGGTGTGTGAGGAGGGGGCGGGATCCCCACCGTCCTGCAGGGCCACATCGACTGTGG
CTCCCTGCTTGGCTACCGCGCTGTCTACCGCATGTGCTTCGCCACGGCGGCCTTCTTCTTCT
TCTTTTTTACCCTGCTCATGCTCTGCGTGAGCAGCAGCCGGGACCCCCGGGCTGCCATCCAG
AATGGGTTTTGGTTCTTTAAGTTCCTGATCCTGGTGGGCCTCACCGTGGGTGCCTTCTACAT
CCCTGACGGCTCCTTCACCAACATCTGGTTCTACTTCGGCGTCGTGGGCTCCTTCCTCTTCA
TCCTCATCCAGCTGGTGTGCTCATCGACTTTGCGCACTCCTGGAACCAGCGGTGGCTGGGC
AAGGCCGAGGAGTGCGATTCCCGTGCTGGTACGCAGGCCTCTTCTTCTTCACTCTCCTCTT
CTACTTGCTGTGATCGCGGCCGTGGCGCTGATGTTTCATGTACTACACTGAGCCCAGCGGCT
GCCACGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCT
GCTGTCTTGCCCAAGGTCCAGGACGCCCAGCCCAACTCGGGTCTGCTGCAGGCCTCGGTCTAT
CACCTCTACACCATGTTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCA
ACCCCCATTTGCCAACCAGCTGGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAG
ACCCAGTGGTGGGATGCCCCGAGCATTGTGGGCCTCATCATCTTCCTCCTGTGCACCCTCTT
CATCAGTCTGCGCTCCTCAGACCACCGGCAGGTGAACAGCCTGATGCAGACCGAGGAGTGCC
CACCTATGCTAGACGCCACACAGCAGCAGCAGCAGCAGGTGGCAGCCTGTGAGGGCCGGGCC
TTTGACAACGAGCAGGACGGCGTCACCTACAGCTACTCCTTCTTCCACTTCTGCCTGGTGCT
GGCCTCACTGCACGTATGATGACGCTCACCAACTGGTACAAGCCCGGTGAGACCCGGAAGA
TGATCAGCACGTGGACCGCCGTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCTCCTC
TACCTGTGGACCCTGGTAGCCCCACTCCTCCTGCGCAACCGCGACTTCAGCTGAGGCAGCCT
CACAGCCTGCCATCTGGTGCCTCCTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACCT
GCCCCCTCCCCACACCAATCAGCCAGGCTGAGCCCCCACCCTGCCCCAGCTCCAGGACCTG
CCCCTGAGCCGGGCCTTCTAGTCGTAGTGCCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCA
GAGCCCCATCCCCCGCCACACCCACACGGTGGAGCTGCCTCTTCCTTCCCCCTCCTCCCTGT
TGCCATACTCAGCATCTCGGATGAAAGGGCTCCCTTGTCTCAGGCTCCACGGGAGCGGGG
CTGCTGGAGAGAGCGGGGAACTCCCACCACAGTGGGGCATCCGGCACTGAAGCCCTGGTGT
CCTGGTCACGTCCCCCAGGGGACCCTGCCCCCTCCTGGACTTCGTGCCTTACTGAGTCTCT
AAGACTTTTTCTAATAAACAAGCCAGTGCGTGTAACAAAAA

FIGURE 9

MGACLGACSLLSASCCLCGSAPCILCSCCPASRNSTVSRLIFTFFLFLGVLVSIIMLSPGVE
SPLYKLPWVCEEAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFFFTLLMLCVSSSRD
PRAAIQNGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSFLFILIQLVLLIDFAHSW
NQRWLKAEECDSRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFC
VCVSIAAVLPKVQDAQPNSSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVA
GPEGYETQWWDAPSIIVGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQQVA
ACEGRAFDNEQDGVITYSYFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVVVKICAS
WAGLLLYLWTLVAPLLLLNRDFS

Signal sequence:

amino acids 1-20

Transmembrane domains:

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,
272-283, 324-340, 391-406, 428-444

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TOSTOT" 4878/660

FIGURE 10

GAGCGAGGCCGGGGACTGAAGGTGTGGGTGTGAGCCCTCTGGCAGAGGGTTAACCTGGGTC
AAATGCACGGATTCTCACCTCGTACAGTTACGCTCTCCCGCGGCACGTCCGCGAGGACTTGA
AGTCCTGAGCGCTCAAGTTTGTCCGTAGGTCGAGAGAAGGCCATGGAGGTGCCGCCACCGGC
ACCGCGGAGCTTTCTCTGTAGAGCATTGTGCCTATTTCCCCGAGTCTTTGCTGCCGAAGCTG
TGACTGCCGATTTCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCC
TATTACCCGGAATCTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAG
AATTTCAAAGGACCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGG
TGTATGGGGGAATACCAGCTTTTATTTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCA
GAAATTTATCATAACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTT
CATTCGTTATGGCTGGCGCTGGGGTTGGAGAACTGCAGTGTTTGTGACTATATTCAACACAG
TGAACACTAGTCTGAATGTATACCGAAATAAAGATGCCTTAAGCCATTTTGTAAATTGCAGGA
GCTGTCACGGGAAGTCTTTTTTAGGATAAACGTAGGCCTGCGTGGCCTGGTGGCTGGTGGCAT
AATTGGAGCCTTGCTGGGCACTCCTGTAGGAGGCCTGCTGATGGCATTTCAGAAGTACGCTG
GTGAGACTGTTTCAGGAAAGAAAACAGAAGGATCGAAAGGCACTCCATGAGCTAAAACTGGAA
GAGTGGAAAGGCAGACTACAAGTTACTGAGCACCTCCCTGAGAAAATTGAAAGTAGTTTACG
GGAAGATGAACCTGAGAATGATGCTAAGAAAATTGAAGCACTGCTAAACCTTCCTAGAAACC
CTTCAGTAATAGATAAACAAGACAAGGACTTGAAAGTGCTCTGAACTTGAAACTCACTGGAGA
GCTGAAGGGAGCTGCCATGTCCGATGAATGCCAACAGACAGGCCACTCTTTGGTCAGCCTGC
TGACAAATTTAAGTGCTGGTACCTGTGGTGGCAGTGGCCTTGCTCTTGTCTTTTTCTTTCTT
TTTAACTAAGAATGGGGCTGTTGTACTCTCACTTTACTTATCCTTAAATTTAAATACATACT
TATGTTTGTATTAATCTATCAATATATGCATACATGGATATATCCACCCACCTAGATTTTAA
GCAGTAAATAAAACATTTTCGCAAAAGATTAAAGTTGAATTTTACAGTTT

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FIGURE 11

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23318

><subunit 1 of 1, 285 aa, 1 stop

><MW: 32190, pI: 9.03, NX(S/T): 2

MEVPPPAPRSFLCRALCLFPRVFAAEAVTADSEVLEERQKRLPYVPEPYYPESGWDRLRELF
GKDEQQRISKDLANICKTAATAGIIGWVYGGIPAFIHAKQQYIEQSQAIEYHNRFDAVQSAH
RAATRGFIRYGWRWGWRTAVFVTIFNTVNTSLNVYRNKDALSHFVIAGAVTGSLFRINVGLR
GLVAGGIIGALLGTPVGGLLMAFQKYAGETVQERKQKDRKALHELKLEEWKGRQLQVTEHLPE
KIESSLREDEPENDAKKIEALLNLPRNPSVIDKQDKD

Important Features:

Signal Peptide:

amino acids 1-24

Transmembrane domains:

amino acids 76-96 and 171-195

N-glycosylation site:

amino acids 153-156

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FIGURE 12

CGGAAGTCCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA
ATCTGGATGGGACCGCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGGA
CCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGAA
TACCAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATCAT
AACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTTCATTCGTTTCATG
GCTGGCGCCGAACC

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FIGURE 13

TCAAGTTTGTCCGTAGGTCGAGAGAAGGCCATGGAGGTGCCGCCACCGGCACCGCGGAGCTT
TTTTCTGTAGAGCATTGTGCCTATTTCCCCGAGTTTTTGTGCTGCCGAAGCTGTGACTGCCGAT
TCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA
ATTTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGG
ACCTTGCTGATATNTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGA
ATACCAGCTTTTATTTCATGNTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATNA
TAACC

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FIGURE 14

GAGCCGCCGCCGCGCGCGCGCCGCGCACTGCAGCCCCAGGCCCGGCCCGCCACCCACGTCT
GCGTTGCTGCCCCGCCTGGGCCAGGCCCAAAGGCAAGGACAAAGCAGCTGTCAGGGAACCT
CCGCCGGAGTCGAATTTACGTGCAGCTGCCGGCAACCACAGGTTCCAAGATGTTTGCGGGG
GCTTCGCGTGTTCCAAGAACTGCCTGTGCGCCCTCAACCTGCTTTACACCTTGGTAGTCTG
CTGCTAATTGGAATTGCTGCGTGGGGCATTGGCTTCGGGCTGATTTCCAGTCTCCGAGTGGT
CGGCGTGGTCATTGCAGTGGGCATCTTCTTGTTCTTGATTGCTTTAGTGGGTCTGATTGGAG
CTGTAAACATCATCAGGTGTTGCTATTTTTTTATATGATTATTCTGTACTTGTATTTATT
GTTCAGTTTTCTGTATCTTGCGCTTGTTTAGCCCTGAACCAGGAGCAACAGGGTCAGCTTCT
GGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAATCTAACTGCT
GTGGGTTCCGAAGTGTTAACCCAAATGACACCTGTCTGGCTAGCTGTGTTAAAAGTGACCAC
TCGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGAGATTTGTTGG
TGGCATTGGCCTGTTCTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACCTACAGATACA
GGAACCAGAAAGACCCCCGCGCAATCCTAGTGCAATTCCTTTGATGAGAAAACAAGGAAGAT
TTCCTTTCGTATTATGATCTTGTTCACTTCTGTAAATTTCTGTAAAGCTCCATTTGCCAGT
TTAAGGAAGGAAACACTATCTGGAAAAGTACCTTATTGATAGTGGAATTATATATTTTTACT
CTATGTTTCTCTACATGTTTTTTCTTTCCGTTGCTGAAAAATATTTGAACTTGTGGTCTC
TGAAGCTCGGTGGCACCTGGAATTTACTGTATTCATTGTCGGGCACTGTCCACTGTGGCCTT
TCTTAGCATTTTTACCTGCAGAAAACTTTGTATGGTACCACTGTGTTGGTTATATGGTGAA
TCTGAACGTACATCTCACTGGTATAATTATATGTAGCACTGTGCTGTGTAGATAGTTCCTAC
TGGAAAAAGAGTGGAATTTATTAAAATCAGAAAGTATGAGATCCTGTTATGTTAAGGGAAA
TCCAAATTCCCAATTTTTTTTTGGTCTTTTTTAGGAAAGATTGTTGTGGTAAAAAGTGTTAGTA
TAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAAATAGTTAT
GTCTTAGGAAATTGTGGTTTAATTTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTGGTTT
CATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCATCAGAATGGAACGAGTTT
TGAGTAATCAGGAAGTATATCTATATGATCTTGATATTGTTTTATAATAATTTGAAGTCTAA
AAGACTGCATTTTTTAAACAAGTTAGTATTAATGCGTTGGCCACGTAGCAAAAAGATATTTG
ATTATCTTAAAAATTGTAAATACCGTTTTCATGAAATTTCTCAGTATTGTAACAGCAACTT
GTCAAACCTAAGCATATTTGAATATGATCTCCATAATTTGAAATTGAAATCGTATTGTGTG
GCTCTGTATATTCTGTAAAAAATTAAAGGACAGAAACCTTTCTTGTGTATGCATGTTTGA
ATTAAAAGAAAGTAATGGAAG

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FIGURE 15

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39979

><subunit 1 of 1, 204 aa, 1 stop

><MW: 22147, pI: 8.37, NX(S/T): 3

MVCGGFACSKNCLCALNLLYTLVSLLLIGIAAWGIGFGLISSLRVVGVIIVGIFLFLIALV
GLIGAVKHHQVLLFFYMIILLLVFIVQFSVSCACLALNQEQQGQLLEVGNNTASARNDIQR
NLNCCGFRSVNPNDTCLASCVKSDHSCSPCAPIIGEYAGEVLRVFGGIGLFFSFTEILGVWL
TYRYRNQKDPRANPSAFL

Signal Peptide:

amino acids 1-34

Transmembrane domains:

amino acids 47-63, 72-95 and 162-182

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FIGURE 16

TGATTGGAGCTGTAAAAAANTCTTCAGGTGTTGTNATTTTTTTTATATGATTATTCTGTAANT
TGTATTTATTGTTTCAGTTTTNTGTATCTTGCGCTTGTTTAGCCNTGAACCAGGAGCAACAGG
GTCAGNTTNTGGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAAT
NTAAACTGCTGTGGGTTCCGAAGTGTTAACCCTGACACCTGTNTGGCTAGCTGTGTTAA
AAGTGACCACTNGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGA
GATTTGTTGGTGGCATTGGCCTGTTNTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACC
TACAGATACAGGAACCAG

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FIGURE 17

AATCCCAAATTCCCCAATTTTTTTGGNCTTTTATAGGGAAAGATGTGTTGTGGTAAAAAGTGT
TAGTATAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAATAG
TTATGTCTTAGGAAATTGTGGTTTAATTTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTG
GTTTCATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCCATCAGAATGGAACG
AGTTTTGAGTAATCCAGGAAGTATATCTATATGATCTTGATATTGTTTTATATAATTTGAAG
TCTAAAAGACTGCATTTTTTAAACAAGTTAGTATTAATGCGTTGGCCCACGTAGCAAAAAGAT
ATTTGATTATCTTAAAAATTGTTAAATACCGTTTTTCATGAAAGTTCTCAGTATTGTAACAGC
AACTTGTCAAACCTAAGCATATTTGAATATGATCTCCCATATTTGAAATTGAAATCGTATT
GTGTGGAGGAAATGGCAATCTTATGTGTGCTGAAGGACACAGTAAGAGCACCAAGTTGTGCC
CCTTGC

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FIGURE 18

ATGATTATTCTGTTACTTGTATTTATTGTTTCAGTTTTATGGTATCTTGCGCTTGTTTTAGCCC
CTGAAACCAGGAGCAACAGGGNNCAGCTTCCTGGAGGTTGGTTGGCAACAATCACGGCCAAG
TGACTCCGCAAATGACATCCCAGAGAAATCCTAAACTGCTGTGGGTTCCGAAGTGTTAACCC
AAATGACACCTGTCTGGCTNGCTGTGTTAAAAGTGACCACTCGTGCTCGCCATGTGCTCCAA
TCATAGGAGAATATGC

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FIGURE 19

CAGTCACCATGAAGCTGGGCTGTGTCCTCATGGCCTGGGCCCTCTACCTTTCCCTTGGTGTG
CTCTGGGTGGCCCAGATGCTACTGGCTGCCAGTTTTGAGACGCTGCAGTGTGAGGGACCTGT
CTGCACTGAGGAGAGCAGCTGCCACACGGAGGATGACTTGACTGATGCAAGGGAAGCTGGCT
TCCAGGTCAAGGCCTACACTTTTCAGTGAACCCTTCCACCTGATTGTGTCTATGACTGGCTG
ATCCTCCAAGGTCCAGCCAAGCCAGTTTTTTGAAGGGGACCTGCTGGTTCTGCGCTGCCAGGC
CTGGCAAGACTGGCCACTGACTCAGGTGACCTTCTACCGAGATGGCTCAGCTCTGGGTCCCC
CCGGGCCTAACAGGGAATTCTCCATCACCGTGGTACAAAAGGCAGACAGCGGGCACTACCAC
TGCAGTGGCATCTTCCAGAGCCCTGGTCTGGGATCCCAGAAACAGCATCTGTTGTGGCTAT
CACAGTCCAAGAACTGTTTCCAGCGCCAATTCTCAGAGCTGTACCCTCAGCTGAACCCCAAG
CAGGAAGCCCCATGACCCTGAGTTGTGAGACAAAGTTGCCCTGCAGAGGTGAGCTGCCCCG
CTCCTCTTCTCCTTCTACAAGGATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAATT
CCAGATCCCCACAGCTTCAGAAGATCACTCCGGGTGATACTGGTGTGAGGCAGCCACTGAGG
ACAACCAAGTTTGGAAACAGAGCCCCCAGCTAGAGATCAGAGTGCAGGGTGCTTCCAGCTCT
GCTGCACCTCCCACATTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGAACTGCTCCTGA
GGAGGCCCTTGGGCTCTGCCTCCGCCGCCAACCCCATCTTCTGAGGATCCAGGCTTTTTCTT
CTCCTCTGGGGATGCCAGATCCTCATCTGTATCACCAGATGGGCCTTCTTCTCAAACACATG
CAGGATGTGAGAGTCTCCTCGGTACCTGCTCATGGAGTTGAGGGAATTATCTGGCCACCA
GAAGCCTGGGACCACAAAGGCTACTGCTGAATAGAAGTAAACAGTTCATCCATGATCTCACT
TAACCACCCCAATAAATCTGATTCTTTATTTTCTCTTCTGTCCTGCACATATGCATAAGTA
CTTTTACAAGTTGTCCCAGTGTTTTGTTAGAATAATGTAGTTAGGTGAGTGTAATAAATTT
ATATAAAGTGAGAATTAGAGTTTAGCTATAATTGTGTATTCTCTCTTAACACAACAGAATTC
TGCTGTCTAGATCAGGAATTTCTATCTGTTATATCGACCAGAATGTTGTGATTTAAAGAGAA
CTAATGGAAGTGGATTGAATACAGCAGTCTCAACTGGGGGCAATTTTGCCCCCAGAGGACA
TTGGGCAATGTTTGGAGACATTTTGGTCATTATACTTGGGGGGTTGGGGGATGGTGGGATGT
GTGTCTACTGGCATCCAGTAAATAGAAGCCAGGGGTGCCGCTAAACATCCTATAATGCACAG
GGCAGTACCCCAACGAAAAATAATCTGGCCCCAAATGTCAGTTGTACTGAGTTTGAGAAA
CCCCAGCCTAATGAAACCCTAGGTGTTGGGCTCTGGAATGGGACTTTGTCCCTTCTAATTAT
TATCTCTTTCCAGCCTCATTGAGCTATTCTTACTGACATAACCAGTCTTTAGCTGGTGCTATG
GTCTGTTCTTTAGTTCTAGTTTGTATCCCCTCAAAGCCATTATGTTGAAATCCTAATCCCC
AAGGTGATGGCATTAAAGAAGTGGGCCTTTGGGAAGTGATTAGATCAGGAGTGCAGAGCCCTC
ATGATTAGGATTAGTGCCCTTATTTAAAAAGGCCCCAGAGAGCTAACTCACCTTCCACCAT
ATGAGGACGTGGCAAGAAGATGACATGTATGAGAACCACAAAAACAGCTGTCGCCAACACCG
ACTCTGTCGTTGCCTTGATCTTGAACCTCCAGCCTCCAGAACTATGAGAAATAAAATTTCTGG
TTGTTTGTAGCCTAA

09978187-101504

FIGURE 20

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40594

><subunit 1 of 1, 359 aa, 1 stop

><MW: 38899, pI: 5.21, NX(S/T): 0

MKLGCVLMAWALYLSLGVWVAQMLLAASFETLQCEGPVCTEESSCHTEDDLTDAREAGFQV
KAYTFSEPFHLIVSYDWLILQGPAKPVFEGDLLVLRCAWQDWPLTQVTFYRDGSALGPPGP
NREFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGS
PMTLSCQTKLPLQRSAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQ
VWKQSPQLEIRVQGASSAAPTTLNPAPQKSAAPGTAPPEAPGPLPPPPTPSSDPGFSSPL
GMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE

Signal sequence:

amino acids 1-17

Leucine zipper pattern sequence:

amino acids 12-33

Protein kinase C phosphorylation site:

amino acids 353-355

09978187 101501
T05T0T 13T3660

FIGURE 21

CCCACGCGTCCGCCCACGCGTCCGCCCACGGGTCCGCCCACGCGTCCGGGCCACCAGAAGTT
TGAGCCTCTTTGGTAGCAGGAGGCTGGAAGAAAGGACAGAAGTAGCTCTGGCTGTGATGGG
ATCTTACTGGGCCTGCTACTCCTGGGGCACCTAACAGTGGACACTTATGGCCGTCCCATCCT
GGAAGTGCCAGAGAGTGTAAACAGGACCTTGGAAAGGGGATGTGAATCTTCCCTGCACCTATG
ACCCCTGCAAGGCTACACCCAAGTCTTGGTGAAGTGGCTGGTACAACGTGGCTCAGACCCT
GTCACCATCTTTCTACGTGACTCTTCTGGAGACCATATCCAGCAGGCAAAGTACCAGGGCCG
CCTGCATGTGAGCCACAAGGTTCCAGGAGATGTATCCCTCCAATTGAGCACCCCTGGAGATGG
ATGACCGGAGCCACTACACGTGTGAAGTCACCTGGCAGACTCCTGATGGCAACCAAGTCGTG
AGAGATAAGATTACTGAGCTCCGTGTCCAGAACTCTCTGTCTCCAAGCCCACAGTGACAAC
TGGCAGCGGTTATGGCTTCACGGTGCCCCAGGGAATGAGGATTAGCCTTCAATGCCAGGCTC
GGGGTTCTCCTCCCATCAGTTATATTTGGTATAAGCAACAGACTAATAACCAGGAACCCATC
AAAGTAGCAACCCTAAGTACCTTACTCTTCAAGCCTGCGGTGATAGCCGACTCAGGCTCCTA
TTTCTGCACTGCCAAGGGGCCAGGTTGGCTCTGAGCAGCACAGCGACATTGTGAAGTTTGTGG
TCAAAGACTCCTCAAAGCTACTCAAGACCAAGACTGAGGCACCTACAACCATGACATACCCC
TTGAAAGCAACATCTACAGTGAAGCAGTCCTGGGACTGGACCACTGACATGGATGGCTACCT
TGGAGAGACCAGTGCTGGGCCAGGAAAGAGCCTGCCTGTCTTTGCCATCATCCTCATCATCT
CCTTGTGCTGTATGGTGGTTTTTACCATGGCCTATATCATGCTCTGTTCGGAAGACATCCCAA
CAAGAGCATGTCTACGAAGCAGCCAGGTAAGAAAGTCTCTCCTCTTCCATTTTTTGACCCCGT
CCCTGCCCTCAATTTTGATTACTGGCAGGAAATGTGGAGGAAGGGGGGTGTGGCACAGACCC
AATCCTAAGGCCGGAGGCCTTCAGGGTCAGGACATAGCTGCCTTCCCTCTCTCAGGCACCTT
CTGAGGTTGTTTTGGCCCTCTGAACACAAAGGATAAATTTAGATCCATCTGCCTTCTGCTTCC
AGAATCCCTGGGTGGTAGGATCCTGATAATTAATTGGCAAGAATTGAGGCAGAAGGGTGGGA
AACCAGGACCACAGCCCCAAGTCCCTTCTTATGGGTGGTGGGCTCTTGGGCCATAGGGCACA
TGCCAGAGAGGCCAACGACTCTGGAGAAACCATGAGGGTGGCCATCTTCGCAAGTGGCTGCT
CCAGTGATGAGCCAACCTTCCCAGAATCTGGGCAACAACCTACTCTGATGAGCCCTGCATAGGA
CAGGAGTACCAGATCATCGCCAGATCAATGGCAACTACGCCCGCCTGCTGGACACAGTTCC
TCTGGATTATGAGTTTCTGGCCACTGAGGGCAAAGTGTCTGTATAAAATGCCCCATTAGGC
CAGGATCTGCTGACATAATTGCCTAGTCAGTCCTTGCCTTCTGCATGGCCTTCTTCCCTGCT
ACCTCTCTTCCCTGGATAGCCCAAAGTGTCCGCCTACCAACACTGGAGCCGCTGGGAGTCACT
GGCTTTGCCCTGGAATTTGCCAGATGCATCTCAAGTAAGCCAGCTGCTGGATTTGGCTCTGG
GCCCTTCTAGTATCTCTGCCGGGGGCTTCTGGTACTCCTCTCTAAATACCAGAGGGAAGATG
CCCATAGCACTAGGACTTGGTCATCATGCCTACAGACACTATTCAACTTTGGCATCTTGCCA
CCAGAAGACCCGAGGGAGGCTCAGCTCTGCCAGCTCAGAGGACCAGCTATATCCAGGATCAT
TTCTCTTTCTTCAAGGGCCAGACAGCTTTTAATTGAAATTGTTATTTACAGGCCAGGGTTCA
GTTCTGCTCCTCCACTATAAGTCTAATGTTCTGACTCTCTCCTGGTGCTCAATAAATATCTA
ATCATAACAGC

09978187-101501

FIGURE 22

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45416

><subunit 1 of 1, 321 aa, 1 stop

><MW: 35544, pI: 8.51, NX(S/T): 0

MGILLGLLLLLGHLLTVDTYGRPILEVPESVTGPGWGDVNLPCYDPLQGYTQVLVKWLVQRGS
DPVTIFLRDSSGDHIQQAKYQGRHLVSHKVPDVSLLQLSTLEMDDRSYHTCEVTWQTPDGNQ
VVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRIQLQCQARGSPPISYIWKQQTNNQE
PIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTKTEAPTTMT
YPLKATSTVKQSWDWTDDMDGYLGGETSAGPGKSLPVFAIILIISLCCMVVFTMAYIMLCRKT
SQQEHVYEAAAR

Signal Sequence:

amino acids 1-19

Glycosaminoglycan attachment site:

amino acids 149-152

Transmembrane domain:

amino acids 282-300

09978187-101501
TOTOT-2382660

FIGURE 23

GCGCCGGGAGCCCATCTGCCCCCAGGGGACGCGGGGCGCGGGGCCGGCTCCCGCCCCGGCACAT
GGCTGCAGCCACCTCGCGCGCACCCCGAGGCGCGCGCCAGCTCGCCCGAGGTCCGTGCGA
GGCGCCCGGCCGCCCCGGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCGTCCGGGGATC
GGGATGTCCCTCCTCCTTCTCCTCTTGCTAGTTTCTACTATGTTGGAACCTTGGGGACTCA
CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTTGCCCTGCCACCATCAACTGGGGC
TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAGGGAACCAAAAA
GTGGTGATCACTTACTCCAGTCGTCTGTCTACAATAACTTGACTGAGGAACAGAAGGGCCG
AGTGGCCTTTGCTTCCAATTTCTTGGCAGGAGATGCCTCCTTGCAGATTGAACCTCTGAAGC
CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTCAGGGCGCTACGTGTGGAGCCAT
GTCATCTTAAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC
AGAAGGAAGTGACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCCATTGTGTATT
ACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGGATGAACGTCTGCCTCCCAAATCTAGGATT
GACTACAACCACCCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCCTACTCTGGACTGTA
CCAGTGACACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCGAGTAACTGTACAGT
ATGTACAAAGCATCGGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTG
ATTTTCCTCCTTGGTGTGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGA
GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAAACCCAGCT
CCTCTTCCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCCTCCACTCGCTCCACAGCAAAT
AGTGCCTCACGCAGCCAGCGGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCCAC
CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAAGAAAGTCCACCATG
CTAATCTGACCAAAGCAGAAACCAACCCAGCATGATCCCCAGCCAGAGCAGAGCCTTCCAA
ACGGTCTGAATTACAATGGACTTGACTCCACGCTTTCCTAGGAGTCAGGGTCTTTGGACTC
TTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCA
GTGAGCATTGCACGGAACAGATTCAGATGAGCATTTCCTTATACAATAACCAACAAGCAAA
AGGATGTAAGCTGATTCATCTGTAAAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGG
AAAGCAGGAGTCCAAATCTATTTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTG
AGGTGAATATACCTAAAACCTTTTAATGTGGGATATTTTGTATCAGTGCTTTGATTACAAAT
TTCAAGAGGAAATGGGATGCTGTTTGTAATTTTCTATGCATTTCTGCAAACCTTATTGGATT
ATTAGTTATTTCAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTAC
TGAGCTAACCACCTTCTAAGAACTCCAAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC
TTCATTTGTCATAAGGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA
AGAGTGAATGAGTTTCTCCCACTCTATACTAATCTCACTATTTGTATTGAGCCCAAATAAC
TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTCCATCTTCATGATGTT
ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTTCCCCTCAAAT
CAGATGCCTCTAAGGACTTTCCTGCTAGATATTTCTGGAAGGAGAAAATACAACATGTCATT
TATCAACGTCCTTAGAAAGAATTCTTCTAGAGAAAAAGGGATCTAGGAATGCTGAAAGATTA
CCCAACATACCATTATAGTCTCTTCTTTCTGAGAAAATGTGAAACCAGAATTGCAAGACTGG
GTGGACTAGAAAGGGAGATTAGATCAGTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA
TGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC
ATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLLVSYYVGTGLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELTEGSDLTLCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLTMSSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSSGSRSSRSGSSSTRSTANS
ASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

09978487-101501
FOSTOT 2832660

FIGURE 25

GTCGTTCCCTTTGCTCTCTCGCGCCAGTCCCTCCCTCGTTCTCCTCAGCCGCTGTGCGAGGAGAGCACCCGGA
 GACGCGGGCTGCAGTCGCGGCGGCTTCTCCCCGCTGGGCGGCCTCGCCGCTGGGCAGGTGCTGAGCGCCCCTAG
 AGCCTCCCTTGCCGCTCCCTCCTCTGCCCCGCGCAGCAGTGACATGGGGTGTGGAGGTAGATGGGCTCCCG
 GCCCCGGAGGCGCGGTGGATGCGGCGCTGGGCAGAAGCAGCCGCGATTCCAGCTGCCCGCGCGCCCCGGGCG
 CCCCTGCGAGTCCCCGGTTTCCAGCCATGGGGACCTCTCCGAGCAGCAGCACCGCCCTCGCCTCCTGCAGCCGCATC
 GCCCCCGAGCCACAGCCACGATGATCGCGGGCTCCCTTCTCCTGCTTGGATTCTTAGCACCACCACAGCTCAG
 CCAGAACAGAAGGCCTCGAATCTCATTTGGCACATACCGCCATGTTGACCGTGCCACCGGCCAGGTGCTAACCTGT
 GACAAGTGTCCAGCAGGAACCTATGTCTCTGAGCATTGTACCAACACAAGCCTGCGCGTCTGCAGCAGTTGCCCT
 GTGGGGACCTTTACCAGGACGAGATGGCATAGAGAATGCCATGACTGTAGTCAGCCATGCCATGGCCATG
 ATTGAGAAATTACCTTGTGCTGCCTTGACTGACCGAGAATGCACTTGCCACCTGGCATGTTCCAGTCTAACGCT
 ACCTGTGCCCCCATACGGTGTGTCTGTGGGTTGGGGTGTGCGGAAGAAAGGGACAGAGACTGAGGATGTGCGG
 TGTAAAGCAGTGTGCTCGGGGTACCTTCTCAGATGTGCCTTCTAGTGTGATGAAATGCAAAGCATACACAGACTGT
 CTGAGTCAGAACCTGGTGGTGATCAAGCCGGGGACCAAGGAGACAGACAACGTCTGTGGCACACTCCCGTCCCTC
 TCCAGCTCCACCTCACCTTCCCCTGGCACAGCCATCTTCCACGCCCTGAGCACATGGAAACCCATGAAGTCCCT
 TCCTCCACTTATGTTCCCAAAGGCATGAATCAACAGAATCCAATCTTCTGCCTCTGTTAGACCAAAGGTACTG
 AGTAGCATCCAGGAAGGGACAGTCCCTGACAAACACAAGCTCAGCAAGGGGGAAGGAAGACGTGAACAAGACCCTC
 CCAAACCTTCAGGTAGTCAACCACCAGCAAGGCCCCACCACAGACACATCCTGAAGCTGCTGCCGTCCATGGAG
 GCCACTGGGGGCGAGAAGTCCAGCACGCCCATCAAGGGCCCCAAGAGGGGACATCCTAGACAGAACCTACACAAG
 CATTTTGACATCAATGAGCATTGCCCCGGATGATTGTGCTTTTCTGCTGCTGGTGCTTGTGGTGAATTGTGGTG
 TGCAGTATCCGGAAGGCTCGAGGACTCTGAAAAAGGGGCCCCGGCAGGATCCAGTGCCATTGTGGAAAGGCA
 GGGCTGAAGAAATCCATGACTCCAACCCAGAACCGGGAGAAATGGATCTACTACTGCAATGGCCATGGTATCGAT
 ATCCTGAAGCTTGTAGCAGCCCAAGTGGGAAGCCAGTGGAAAGATATCTATCAGTTTCTTTGCAATGCCAGTGAG
 AGGGAGGTTGCTGCTTTTCTCAATGGGTACACAGCCGACCACGAGCGGGCTACGCAGCTCTGCAGCACTGGACC
 ATCCGGGGCCCCGAGGCCAGCCTCGCCAGCTAATTAGCGCCCTGCGCCAGCACCGGAGAAACGATGTTGTGGAG
 AAGATTCTGTTGGGCTGATGGAAGACACCACCCAGCTGGAACCTGACAACTAGCTCTCCCGATGAGCCCCAGCCCCG
 CTAGCCCCGAGCCCCATCCCCAGCCCCAACCGGAACTTGAGAATTCCGCTCTCCTGACGGTGGAGCCTTCCCCA
 CAGGACAAGAACAAGGGCTTCTTCTGATGAGTCCGAGCCCCCTTCTCCGCTGTGACTCTACATCCAGCGGCTCC
 TCCGCGCTGAGCAGGAACGGTTCTTTATTACCAAAGAAAGAAAGGACACAGTGTGCGGCAGGTACGCCTGGAC
 CCCTGTGACTTGCAGCCTATCTTTGATGACATGCTCCACTTTCTAAATCCTGAGGAGCTGCGGGTGAATTGAAGAG
 ATTCCCCAGGCTGAGGACAACTAGACCGGCTATTTCGAAATTATTGGAGTCAAGAGCCAGGAAGCCAGCCAGACC
 CTCCTGGACTCTGTTTATAGCCATCTTCTGACCTGCTGTAGAACATAGGGATACTGCATTCTGGAAATTACTCA
 ATTTAGTGGCAGGGTGGTTTTTTAATTTCTTCTGTTTCTGATTTTTGTGTTTGGGGTGTGTGTGTGTTTTGT
 GT
 TCTCTCTCTTTTTTTTTTTAAATAACTCTTCTGGGAAGTTGGTTTTATAAGCCTTTGCCAGGTGTAACCTGTTGTGAA
 ATACCCACCCTAAAGTTTTTTAAGTTCCATATTTTCTCCATTTTGCCTTCTTATGTATTTTCAAGATTATTCTG
 TGCATTTTAAATTTACTTAACTTACCATAAATGCAGTGTGACTTTTCCACACACTGGATTGTGAGGCTCTTAAC
 TTCTTAAAGTATAATGGCATCTTGTGAATCCTATAAGCAGTCTTTATGTCTCTTAACATTACACCTACTTTTT
 AAAAACAAATATTATTACTATTTTTATTATTGTTTGTCTTTATAAAATTTCTTAAAGATTAAGAAAAATTTAAGA
 CCCATTGAGTTACTGTAATGCAATTCAACTTTGAGTTATCTTTAAATATGTCTTGTATAGTTTATATTATCATGG
 CTGAAACTTGACCACACTATTGCTGATTGTATGGTTTTTACCTGGACACCGTGTAGAATGCTTGATTACTTGTAC
 TCTTCTTATGCTAATATGCTCTGGGCTGGAGAAATGAAATCCTCAAGCCATCAGGATTTGCTATTTAAGTGGCTT
 GACAACTGGGCCACCAAAGAACTTGAACCTTACCTTTTAGGATTTGAGCTGTTCTGGAACACATTGCTGCACTTT
 GGAAAGTCAAAATCAAGTGCCAGTGGCGCCCTTTCCATAGAGAATTTGCCAGCTTTGCTTTAAAGATGTCTTG
 TTTTTATATACATAATCAATAGGTCCAATCTGCTCTCAAGGCCCTTGGTCTGGTGGGATTCTTTACCAATTT
 ACTTTAATTAATAATGGCTGCAACTGTAAGAACCTTGTCTGATATATTTGCAACTATGCTCCCATTTACAAATG
 TACCTTCTAATGCTCAGTTGCCAGGTTCCAATGCAAAGGTGGCGTGGACTCCCTTTGTGTGGGTGGGGTGTGTGG
 GTAGTGGTGAAGGACCGATATCAGAAAAATGCCTTCAAGTGTACTAATTTATTAATAAACATTAGGTGTTTGTGA
 AAAAAAAA

09978187-101501

FIGURE 26

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594

><subunit 1 of 1, 655 aa, 1 stop

><MW: 71845, pI: 8.22, NX(S/T): 8

MGTSPSSSTALASCSRIARRATATMIAGSLLLLLGFLSTTTAQPEQKASNLIQTYRHVDRATG
QVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTRHENGIEKCHDCSQPCPWPMIEKLPCA
ALTDRECTCPPGMFQSNATCAPHTVCPVGWGVRRKKGTETEDVRCKQCARGTFSDVPSSVMKC
KAYTDCLSQNLVVIKPGTKETDNVCGTLPSSFSSSTSPSPGTAFPRPEHMETHEVPSSTYVP
KGMNSTESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPNLQVVNHQQGPHHRHIL
KLLPSMEATGGEKSSTPIKGPKRGHPRQNLHKHFDINEHLPWMIVLFLLLVLVVIVVCSIRK
SSRTLKKGPRQDPSAIVEKAGLKKSMTPTQNREKWIYYCNGHGIDILKLVAQAQVGSQWKDIY
QFLCNASEREVAAFSNGYTADHERAYAALQHWTIRGPEASLAQLISALRQHRNDVVEKIRG
LMEDTTQLETDKLALPMSPSPSPSPSPNAKLENSALLTVEPSPQDKNKGFFVDESEPLL
RCDSTSSGSSALSRNGSFITKEKKDTVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQ
AEDKLDRLFEEIGVKSQEASQTLSDSVYSHLPDLL

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 350-370

0978187-1050
TOSTOT/38/66

FIGURE 27

ATGGGAAGCCAGTAACACTGTGGCCTACTATCTCTTCCGTGGTGCCATCTACATTTTTTGGGA
 CTCGGGAATTATGAGGTAGAGGTGGAGGCGGAGCCGGATGTCAGAGGTCTGAAATAGTCAC
CATGGGGGAAAATGATCCGCCTGCTGTTGAAGCCCCCTTCTCATTCGGATCGCTTTTTTGGCC
 TTGATGATTTGAAAATAAGTCCTGTTGCACCAGATGCAGATGCTGTTGCTGCACAGATCCTG
 TCACTGCTGCCATTGAAGTTTTTTTCCAATCATCGTCATTGGGATCATTGCATTGATATTAGC
 ACTGGCCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGAAGTACAGATGTCGCTCATCCT
 TTAAGTGTATCGAGCTGATAGCTCGATGTGACGGAGTCTCGGATTGCAAAGACGGGGAGGAC
 GAGTACCGCTGTGTCCGGGTGGGTGGTCAGAATGCCGTGCTCCAGGTGTTACAGCTGCTTC
 GTGGAAGACCATGTGCTCCGATGACTGGAAGGGTCACTACGCAAATGTTGCCTGTGCCAAC
 TGGGTTTCCCAAGCTATGTGAGTTCAGATAACCTCAGAGTGAGCTCGCTGGAGGGGCAGTTC
 CGGGAGGAGTTTGTGTCCATCGATCACCTCTTGCCAGATGACAAGGTGACTGCATTACACCA
 CTCAGTATATGTGAGGGAGGGATGTGCCTCTGGCCACGTGGTTACCTTGCAGTGCACAGCCT
 GTGGTCATAGAAGGGGCTACAGCTCACGCATCGTGGGTGGAAACATGTCTTGCTCTCGCAG
 TGGCCCTGGCAGGCCAGCCTTCAGTTCAGGGGTACCACCTGTGCGGGGGCTCTGTCATCAC
 GCCCCTGTGGATCATCACTGCTGCACACTGTGTTTATGACTTGTACCTCCCCAAGTCATGGA
 CCATCCAGGTGGGTCTAGTTTCCCTGTTGGACAATCCAGCCCCATCCCACTTGGTGGAGAAG
 ATTGTCTACCACAGCAAGTACAAGCCAAAGAGGCTGGGCAATGACATCGCCCTTATGAAGCT
 GGCCGGGCCACTCACGTTCAATGAAATGATCCAGCCTGTGTGCCTGCCCAACTCTGAAGAGA
 ACTTCCCCGATGGAAAAGTGTGCTGGACGTCAAGATGGGGGGCCACAGAGGATGGAGGTGAC
 GCCTCCCCTGTCTGAACCACGCGGCCGTCCCTTTGATTCCAACAAGATCTGCAACCACAG
 GGACGTGTACGGTGGCATCATCTCCCCCTCCATGCTCTGCGCGGGCTACCTGACGGGTGGCG
 TGGACAGCTGCCAGGGGGACAGCGGGGGGCCCTGGTGTGTCAAGAGAGGAGGCTGTGGAAG
 TTAGTGGGAGCGACCAGCTTTGGCATCGGCTGCGCAGAGGTGAACAAGCCTGGGGTGTACAC
 CCGTGTACCTCCTTCCTGGACTGGATCCACGAGCAGATGGAGAGAGACCTAAAAACCTTGAA
 GAGGAAGGGGACAAGTAGCCACCTGAGTTCCTGAGGTGATGAAGACAGCCCGATCCTCCCCT
 GGACTCCCGTGTAGGAACCTGCACACGAGCAGACACCCTTGGAGCTCTGAGTTCGGGCACCA
 GTAGCAGGCCCCGAAAGAGGCACCCTTCCATCTGATTCCAGCACAACCTTCAAGCTGCTTTTT
 GTTTTTTTGTTTTTTTGAAGGTGGAGTCTCGCTCTGTTGCCCAGGCTGGAGTGCAGTGGCGAAA
 TCCCTGCTCACTGCAGCCTCCGCTTCCCTGGTTCAAGCGATTCTCTTGCCCTCAGCTTCCCCA
 GTAGCTGGGACCACAGGTGCCCCGCCACCACACCCAACTAATTTTTTGTATTTTTTAGTAGAGAC
 AGGGTTTCACCATGTTGGCCAGGCTGCTCTCAAACCCCTGACCTCAAATGATGTGCCTGCTT
 CAGCCTCCCACAGTGCTGGGATTACAGGCATGGGCCACCACGCCTAGCCTCACGCTCCTTTC
 TGATCTTCACTAAGAACAAAAGAAGCAGCAACTTGCAAGGGCGGCCTTCCCCTGGTCCAT
 CTGGTTTTCTCTCCAGGGTCTTGCAAAATTCCTGACGAGATAAGCAGTTATGTGACCTCACG
 TGCAAAGCCACCAACAGCCACTCAGAAAAGACGCACCAGCCCAGAAGTGCAGAACTGCAGTC
 ACTGCACGTTTTTCATCTCTAGGGACCAGAACCACCAACCCACCCTTCTACTTCCAAGACTTAT
 TTTCACATGTGGGGAGGTTAATCTAGGAATGACTCGTTTAAGGCCTATTTTCATGATTTCTT
 TGTAGCATTTGGTGCTTGACGTATTATTGTCTTTGATTCCAATAATATGTTTCTTCCCT
 CATTGTCTGGCGTGTCTGCGTGGACTGGTGACGTGAATCAAATCATCCACTGAAA

0978137 101501

FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45234

><subunit 1 of 1, 453 aa, 1 stop

><MW: 49334, pI: 6.32, NX(S/T): 1

MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALILA
LAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVFTAAS
WKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIHLLPDDKVTALHH
SVYVREGCASGHVVTLOCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVIT
PLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKL
AGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAVPLISNKICNHR
DVYGGIISPSMLCAGYLTGGVDSCQGDSSGGLVCQERRLWKLVGATSFQIGCAEVNKPQVYT
RVTSFLDWIHEQMERDLKT

Signal Peptide:

amino acids 1-20

Transmembrane domain:

amino acids 240-284

0978137 2813660

FIGURE 29

CCCACGCGTCCGTCTTAGTCCCCGGGCCAACTCGGACAGTTTGCTCATTTATTGCAACGGTCAAGGCTGGCTTGT
GCCAGAACGGCGCGCGCGCACGCACACACACGGGGGAACTTTTAAATGAAAGGCTAGAAGA
GCTCAGCGCGCGCGCGCGCTGCGCGAGGGCTCCGGAGCTGACTCGCCGAGGCAGGAAATCCCTCCGGTCCGGA
CGCCCGGCCCCGGCTCGGCGCCCGCTGGGATGGTGCAGCGCTCGCCCGGGCCGAGAGCTGCTGCACTGAAG
GCCGGCGACGATGCGAGCGCGCCCGTCCCCGTGTCCCCCGCCCGCCCTCCTGCTCGCCCTGGCCGGTGTCT
GCTCGCGCCCTGCGAGGCCCGAGGGGTGAGCTTATGGAACCAAGGAAGAGCTGATGAAGTTGTGAGTGCCTCTGT
TCGGAGTGGGGACCTCTGGATCCCAGTGAAGAGCTTCGACTCCAAGAATCATCCAGAAGTGCTGAATATTCGACT
ACAACGGGAAAGCAAAGAACTGATCATAAATCTGGAAGAAATGAAGGTCTCATTGCCAGCAGTTTACGGAAAC
CCACTATCTGCAAGACGGTACTGATGTCTCCCTCGCTCGAAATTACACGGGTCACTGTTACTACCATTGGACATGT
ACGGGGATATTCTGATTGAGCAGTCACTCTCAGCACGTGTTCTGGTCTCAGGGGACTTATTGTGTTTGAAAATGA
AAGCTATGTCTTAGAACCAATGAAAAGTGCAACCAACAGATACAACTCTTCCCAGCGAAGAAGCTGAAAAGCGT
CCGGGGATCATGTGGATCACATCACACACCAAACTCGCTGCAAGAATGTGTTCCACCACCCTCTCAGAC
ATGGGCAAGAAGGCATAAAGAGAGACCCTCAAGGCAACTAAGTATGTGGAGCTGGTGATCGTGGCAGACAACCG
AGAGTTTTCAGAGGCAAGGAAAAGATCTGGAAGAAAGTTAAGCAGCGATTAAATAGAGATTGCTAATCACGTTGACAA
GTTTTACAGACCACTGAACATTCCGATCGTGTGGTAGGCGTGGAAGTGGAATGACATGGACAAATGCTCTGT
AAGTCAGGACCCATTACCCAGCCTCCATGAATTTCTGGACTGGAGGAAGATGAAGCTTCTACCTCGCAAATCCCA
TGACAATGCGCAGCTTGTGAGTGGGGTTTATTTCCAAGGGACCACCATCGGCATGGCCCCAATCATGAGCATGTG
CACGGCAGACCAGTCTGGGGGAATTGTGATGGACCATTGAGACAATCCCCTTGGTGCAGCCGTGACCCTGGCACA
TGAGCTGGGGCCACAATTTCCGGATGAATCATGACACACTGGACAGGGGCTGTAGCTGTCAAATGGCGGTTGAGAA
AGGAGGCTGCATCATGAACGCTTCCACCGGTACCCATTTCCCATGGTGTTCAGCAGTTGCAGCAGGAAGGACTT
GGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCCTGTTTAACTGCGCGAAGTCAGGGAGTCTTTCGGGGGCCA
GAAGTGTGGGAACAGATTTGTGGAAGGAAGGAGAGGAGTGTGACTGTGGGGAGCCAGAGGAATGTATGAATCGCTG
CTGCAATGCCACCACCTGTACCTGAAGCCGGACGCTGTGTGCGCACATGGGCTGTGCTGTGAAGACTGCCAGCT
GAAGCCTGCAGGAACAGCGTGCAGGGACTCCAGCAACTCCTGTGACCTCCCAGAGTTCTGCACAGGGGGCCAGCCC
TCACTGCCCAGCCAATGTGTACCTGCACGATGGGCACTCATGTGAGGATGTGGACGGCTACTGCTACAATGGCAT
CTGCCAGACTCACGAGCAGCAGTGTGTACGCTCTGGGGACCAGGTGCTAAACCTGCCCCCTGGGATCTGCTTTGA
GAGAGTCAATTCGAGGTGATCCTTATGGCAACTGTGGCAAAGTCTCGAAGAGTTCCTTTGCCAAATGCGAGAT
GAGAGATGCTAAATGTGGAAAAATCCAGTGTCAAGGAGGTGCCAGCCGGCCAGTCATTGGTACCAATGCCGTTTC
CATAGAAACAAACATCCCTCTGCAGCAAGGAGGCCGATTCTGTGCCGGGGGACCCACGTGTACTTGGCGCATGA
CATGCCGGACCCAGGGCTTGTGCTTGCAGGCACAAAGTGTGAGATGGAAAAATCTGCCTGAATCGTCAATGTCA
AAATATTAGTGTCTTTGGGGTTCACGAGTGTGCAATGCAGTGCCACGGCAGAGGGGTGTGCAACAACAGGAAGAA
CTGCCACTGCGAGGCCCCACTGGGCACCTCCCTTCTGTGACAAGTTTGGCTTTGGAGGAAGCACAGACAGCGGCC
CATCCGGCAAGCAGAAGCAAGGCAGGAAGCTGCAGAGTCCAACAGGGAGCGCGCCAGGGCCAGGAGCCCGTGGG
ATCGCAGGAGCATGCGTCTACTGCCTCACTGACACTCATCTGAGGCCCTCCCATGACATGGAGACCGTGACCAGTG
CTGCTGCAGAGGAGGTACGCGTCCCCAAGGCCTCCTGTGACTGGCAGCATTGACTCTGTGGCTTTGCCATCGTT
TCCATGACAACAGACACAACACAGTTCTCGGGGCTCAGGAGGGGAAGTCCAGCCTACCAGGCACGTCTGCAGAAA
CAGTGCAAGGAAGGGCAGCGACTTCTCGTTGAGCTTCTGCTAAAACATGGACATGCTTCACTGCTGCTCCTGAG
AGAGTAGCAGGTTACCACTCTGGCAGGCCCCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAAGTCTGGCCTTTC
ACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTTGGGCCAGTGTCCCCTTCCCCAGTGACACCTCAGCCT
TGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTCTGATATGGCTTTTAGCATTTATTATATGAAAAT
AGCAGGGTTTTAGTTTTTAATTTATCAGAGACCCCTGCCACCCATTCCATCTCCATCCAAGCAAACCTGAATGGCAA
TGAAACAACTGGAGAAGAAGGTAGGAGAAAGGGCGGTGAACTCTGGCTCTTGTGTGGACATGCGTGACCAGC
AGTACTCAGGTTTGAAGGGTTTGAGAAAGCCAGGGAACCCACAGAGTCACCAACCCCTTCATTAAACAAGTAAGAA
TGTTAAAAAGTGAACAATGTAAGAGCCTAACTCCATCCCCCGTGGCCATTACTGCATAAAATAGAGTGCATTT
GAAAT

09973137-101501

FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49624

><subunit 1 of 1, 735 aa, 1 stop

><MW: 80177, pI: 7.08, NX(S/T): 5

MAARPLPVSPARALLLALAGALLAPCEARGVSLWNQGRADEVVSASVRSGLWIIPVKSFDISK
NHPEVLNIRLQRESKELIINLERNEGLIASSFTETHYLQDGTDVSLARNYTGHCCYYHGHVIRG
YSDSAVSLSTCSGLRGLIVFENESYVLEPMKSATNRYKLFPAKKLKSVRGSCGSHHNTPNLA
AKNVFPPPSQTWARRHKRETLKATKYVELVIVADNREFQRQKDKLEKVKQRLIEIANHVDKF
YRPLNIRIVLVGVEVWDMDKCSVSQDPFTSLHEFLDWRKMKLLPRKSHDNAQLVSGVYFQG
TTIGMAPIMSMCTADQSGGIVMDHSDNPLGAAVTLAHELGHNFNGMNHDTLDRGCSCQMAVEK
GGCIMNASTGYPPFMVFSSCSRKDLETSLEKGMGVCLFNLPEVRESFGGQKCGNRFVEEGEE
CDCGEPEECMNRRCCNATTCTLKPDVAHGLCCEDCQLKPAGTACRDSSNSCDLPEFCTGAS
PHCPANVYLHDGHSCQDVGVCYNGICQTHEQQCVTLWGPGAKPAPGICFERVNSAGDPYGN
CGKVSKESSFAKCEMRDAKCGKIQCQGGASRPVIGTNAVSIETNIPLQQGGRILCRGTHVYLG
DDMPDPGLVLGATKCADGKICLNRQCQNI SVFGVHECAMQCHGRGVCNNRKNCHCEAHWAPP
FCDKFGFGGSTDSGPIRQAEARQEAESNRERGGQGEVPGSQEHASTASLTLLI

Signal peptide:

amino acids 1-28

0997187-10504

FIGURE 31

TCCCAAGGCTTCTTGGATGGCAGATGATTNTGGGGTTTTGCATTGTTTCCCTGACAACGAAA
ACAAAACAGTTTTTGGGGGTTTCAGGAGGGGAANTCCAGCCTACCCAGGAAGTTTGCAGAAACA
GTGCAAGGAAGGGCAGGANTTCCTGGTTGAGNTTTTTGNTAAACATGGACATGNTTCAGTG
CTGCTCNTGAGAGAGTAGCAGGTTACCACTTTTGGCAGGCCCCAGCCCTGCAGCAAGGAGGA
AGAGGACTCAAAAGTTTTGGCCTTTCACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTT
GGGCCCAGTGTCCCCTTTCCCCAGTGACACCTCAGCCTTGGCAGCCCTGATAACTGGTNTNT
GGCTGCAANTTAATGCTNTGATATGGCTTTTAGCATTTATTATATGAAAATAGCAGGGTTTT
AGTTTTTAATTTATCAGAGACCCTGCCACCCATTCCATNTCCATCCAAG

09978187-101501

FIGURE 32

CATCCTGCAACATGGTGAAACCACGCCTGGCTAATTTTGTGTATTTTTTGGTAGAGATGGGA
TTTCACCGTGTTAGCCAGGATTGTCTCAATCTGACCTCATGATCTGCCCCCCTCGGCCTCCC
AAAGTGCTGGGATTACAGGCGAGTGCAACCACACCCGGCCACAACTTTTTTAAGAAGTTAAT
GAAACCATAACCTTTTACATTTTTTAATGACAGGAAAATGCTCACAATAATTGTTAACCACAAA
TTCTGGATACAAAAGTACAATCTTTACTGTGTAAATACATGTATATGTACTATATGAAAATA
TACCAAATATCAATAATACTTATCTCTGGGTAAAAACCTCTTCTCATACCCTGTGCTAACAA
CTTTTAACAAAAAATTTGCATCACTTTTAAGAATCAAGAAAAATTTCTGAAGGTCATATGGG
ACAGAAAAAAAACCAAGGGAAAAATCACGCCACTTGGGAAAAAAGATTTCGAAATCTGCCT
TTTTATAGATTTGTAATTAATAAGGTCCAGGCTTTCTAAGCAACTTAAATGTTTTGTTTCGA
AACAAAGTACTTTGTCTGGATGTAGGAGGAAAGGGAGTGATGTCACTGCCATTATGATGCCCC
TTGAATATAAGACCCTACTTGCTATCTCCCCCTGCACCAGCCAGGAGCCACCCATCCTCCAGC
ACACTGAGCAGCAAGCTGGACACACGGCACACTGATCCAAATGGGTAAGGGGATGGTGGCGA
TGCTCATTTCTGGGTCTGCTACTTCTGGCGCTGCTCCTACCCGTGCAGGTTTCTTCATTTGTT
CCTTTAACCAGTATGCCGGAAGCTACTGCAGCCGAAACCACAAAGCCCTCCAACAGTGCCCT
ACAGCCTACAGCCGGTCTCCTTGTGGTCTTGCTTGCCCTTCTACATCTCTACCATTAAAGAGG
CAGGTCAAGAAACAGCTACAGTTCTCCAACCCATACACTAAAACCGAATCCAAATGGTGCCT
AGAAGTTCAATGTGGCAAGGAAAAAAACCAGGTCTTCATCAAATCTACTAATTTCACTCCTT
ATTAACAGAGAAACGCTTGAGAGTCTCAAACCTGGACTGGTTTAAAGAGCATCTGAAGGATTT
GACTAGATGATAAATGCCTGTACTCCAGTACTTTGGGAGGCCTAGGCCGGCGGATCACCTG
AGGTCAGGAGTTTGAGACTAACCTGGCCAAAATGGTGAAACCCCATCTGTACTAAAAATACA
AATATTGACTGGGCGTGGTGGTGAGTGCCTGTGATCCCAGCTACTCAGGTGGCTGAAGCAGG
ACAATCACTTGAACTCAGGAGGCAGAGGTTGCAGTGAGCTGAGATCGCGCTACTGCACTCTA
GCCTAGCCTGGGCAACAGAGTGAGACTTCGTCTCAAAAAAAAAAAAAAGCCAAGTGCAAGTGGCT
CACGCCTGTAATCCCGGCACCTTTGGGAGGCCGAGGTGGGCGGATCACGAGGTCAGGAGATCA
AGACCATCCTGGCTAATACAGTGAAACCCTGTCTCTACTAAAAATACAAAAAATTAGCCGGG
GATGGTGGCAGGCACCTGGAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATAGCGTGAA
CTCAGGAGGCGGAGCTTGCAGTGAGCCGAGATTGCGCTACTGCACTCCAGCCTGGGCGACAG
CGCGAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 33

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48309

><subunit 1 of 1, 67 aa, 1 stop

><MW: 6981, pI: 7.47, NX(S/T): 0

MGKGMVAMLILGLLLLALLLPVQVSSFVPLTSMPEATAAETTKPSNSALQPTAGLLVVLLAL
LHLYH

Signal peptide:

amino acids 15-27

09978187-101501
TOSTOT-28182660

0 9 2 3 6 7 0 1

GCCGCGGCGAGAGCGCGCCACGCCCCGCGCGCGATGCCCGCGCGCCAGGACGCCTCCTCCCGCTGCTGGCCCGGC
 CGGCGGCCCTGACTGCGCTGCTGCTGCTGCTGCTGGGCCATGGCGGCGGCGGGCGCTGGGGCGCCCGGGCCAGG
 AGGCGGCGGCGGCGGCGGCGGACGGGCCCCCGCGGCAGACGGCGAGGACGGACAGGACCCGCACAGCAAGCACCC
 TGTACACGGCCGACATGTTACGCACGGGATCCAGAGCGCCGCGCACTTCGTATGTTCTTCGCGCCCTGGTGTG
 GACACTGCCAGCGGCTGCAGCCGACTTGGAAATGACCTGGGAGACAAATACAACAGCATGGAAGATGCCAAAGTCT
 ATGTGGCTAAAGTGGACTGCACGCGCCCACTCCGACGTGTGCTCCGCCAGGGGTGCGAGGATACCCACCTTAA
 AGCTTTTTCAAGCCAGGCCAAGAAAGCTGTGAAGTACCAGGGTCTTCGGGACTTCAGACACTGGAAAACTGGATGC
 TGCAGACACTGAACGAGGAGCCAGTGCACACCAGAGCCGGAAGTGGAAACCGCCAGTGGCCCCGAGCTCAAGCAAG
 GGCTGTATGAGCTCTCAGCAAGCAACTTTGAGCTGCACGTTGCACAAGGCGACCACTTTATCAAGTTCTTCGCTC
 CGTGGTGTGGTCACTGCAAGCTTGGCTTCCAACTCTGGGAGCAGCTGGCTCTGGGCCCTTGAAACATTCCGAAACTG
 TCAAGATTGGCAAGGTTGATTGTACACAGCATATGAACCTCTGCTCCGAAACAGGTTCTGTGCTATCCCACCT
 TTCTCTGGTTCCGAGATGGGAAAAAGTGGATCAGTACAAGGGAAAGCGGATTTGGAGTCACTGAGGAGTACG
 TGGAGTGCAGCTGCAGCGCACAGAGACTGGAGCGACGGAGACCGTCACGCCCTCAGAGGCCCCGGTGTGGCAG
 CTGAGCCCGAGGCTGACAAGGGCACTGTGTTGGCACTCACTGAAAATAACTTCGATGACACCATTGCAGAAGGAA
 TAACCTTCATCAAGTTTTATGCTCCATGGTGTGGTCATTGTAAGACTCTGGCTCCTACTTTGGGAGGAACTCTCTA
 AAAAGGAATTCCCTGGTCTGGCGGGGGTCAAGATCGCCGAAGTAGACTGCATGCTGCAACGGAATATCTGCAGCA
 AGTATTCGGTACAGGCTACCCCAACGTTATTGCTTTCCGAGGAGGGAAGAAAGTCAGTGAGCAGCTGGAGGCA
 GAGACCTTGACTCGTTACACCGCTTTGCTCTTGAGCCAAGCGAAAGACGAACTTTAGGAACACAGTTGGAGGTAC
 CTCTCCTGCCAGCTCCCGCACCCCTGCGTTTAGGAGTTCAGTCCACAGAGGCCACTGGGTTCCAGTGGTGGCT
 GTTCAGAAAGCAGAACATACTAAGCGTGAGGTATCTTCTTTGTGTGTGTGTTTTCCAAGCCAACACACTCTACAG
 ATTCTTTATTAAAGTTAAGTTTTCTCTAAGTAAATGTGTAACTCATGGTCACTGTGTAAACATTTTCAGTGGCGATA
 TATCCCCCTTGACCTTCTCTTGATGAAATTTACATGGTTTCTTTGAGACTAAATAGCGTTGAGGGAAATGAAA
 TTGCTGGACTAATTTGTGGCTCCTGAGTTGAGTGATTTTGGTGAAAGAAAGCAGATCCAAAGCAGATGTTTACCTGC
 CCACGAGTTCCTGGAAGGTTGGCCTTGTGGCAGTATTGACGTTTCTTGATCTTAAGGTACAGTTGACTCAATAC
 TGTGTTGGTCCGTAGCATGGAGCAGATTGAAATGCAAAACCCACACCTCTGGAAGATACCTTCACGGCCGCTGC
 TGGAGCTTCTGTTGCTGTGAATACTTCTCTCAGTGTGAGAGGTTAGCCGTGATGAAAGCAGCGTTACTTCTGACC
 GTGCCCTGAGTAAGAGAAATGCTGATGCCATAACTTTATGTGTCGATACCTTGTCAAATCAGTTACTGTTTACGGGGAT
 CTTCTGTTTCTCAGGGGTGAAACATGTCTTTAGTTCTCATGTTAACACGAAGCCAGAGCCCACTGAACATGT
 TGGATGCTTCTCTTAGAAAGGGTAGGCATGGAAATTCACAGGGCTCATTCTCAGTATCTCAATTAACCTATTGA
 AAGATTCCAGTTGTATTTGTACCTGGGGTGACAAGACCAGACAGGCTTTCACAGGCCTGGGTATCCAGGGAGGC
 TCTGCAGCCCTGCTGAAGGGCCCTAACTAGAGTTCTAGAGTTTCTGATTCTGTTTCTCAGTAGTCTTTTAGAGG
 CTTGCTATACCTGGTCTGCTTCAAGGAGGTGCACCTTCTAATGTATGAGAATGGGATGCATTTGATCTCAAGAC
 CAAAGACAGATGTCACTGGGCTGCTCTGGCCCTGGTGTGCACGGCTGTGGCAGCTGTTGATGCCAGTGTCTCTTA
 ACTCATGCTGTCTTTGTGATTAAACACCTCTATCTCCTTGGGAAATAAGCACATACAGGCTTAAGCTCTAAGATA
 GATAGGTGTTTGTCTTTTACCATCGAGCTACTTCCCATATAAACCACCTTTCAGTCAACACTTTCACCCACCT
 CCCATACGCAAGGGGATGTGGATACTTGGCCCAAAGTAACTGGTGGTAGGAATCTTAGAAACAAGACCACTTATA
 CTGTCTGTCTGAGGCAGAAGATAACAGCAGCATCTCGACCAGCCTCTGCCTTAAAGGAAATCTTTATTAATCACG
 TATGGTTTCAGAGATAATCTTTTTTTAAAAAAACCCAACTCCTAGAGAAGCACAACTGTCAAGAGTCTTGTACA
 CACAACCTCAGCTTTGTCATCAGAGTCTGTGATTCCAAGAAAATCAAAGTGGTACAATTTGTTTGTTTACACTAT
 GATACTTTCTAAATAAACTCTTTTTTTTTTAA

FIGURE 35

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46776

><subunit 1 of 1, 432 aa, 1 stop

><MW: 47629, pI: 5.90, NX(S/T): 0

MPARPGRLLPLLARPAALTALLLLLLLGHGGGGRWGARAQEAAAAAADGPPAADGEDGQDPHS
KHLYTADMFTHTGIQSAAHFVMFFAPWCGHCQRLQPTWNDLGDKYNSMEDAKVYVAKVDCTAH
SDVCSAQQGVRGYPTLKLFKPGQEAVKYQGPRDFQTLNWMQLQTLNEEPVTPEPEVEPPSAPE
LKQGLYELASNFELHVAQGDHFIKFFAPWCGHCALAPTWEQLALGLEHSETVKIGKVDCT
QHYELCSGNQVRGYPTLLWFRDGKKVDQYKGKRDLESLREYVESQLQRTETGATETVTPSEA
PVLAAEPEADKGTVLALTENNFDDTIAEGITFIKFYAPWCGHCKTLAPTWEELSKKEFPGLA
GVKIAEVDCTAERNICSKYSVRGYPTLLLFRGGKKVSEHSGGRDLDSLHRFVLSQAKDEL

Signal sequence:

amino acids 1-32

09978187.101501

FIGURE 36

CTTTTCTGAGGAACCAACAGCAATGAATGGCTTTGCATCCTTGCTTCGAAGAAACCAATTTAT
CCTCCTGGTACTATTTCTTTTGCAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCCTA
CCGCTGAAGTCTGTGCCACACACACAATTTACCAGGACCCAAAGGAGATGATGGTGAAAAA
GGAGATCCAGGAGAAGAGGGGAAAGCATGGCAAAGTGGGACGCATGGGGCCGAAAGGAATTAA
AGGAGAAGTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCCATTGGGAAGA
AGGGTGACAAAGGGGAAAAAGGTTTGCTTGGAATACCTGGAGAAAAAGGCAAAGCAGGTACT
GTCTGTGATTGTGGAAGATACCGGAAATTTGTTGGACAACCTGGATATTAGTATTGCTCGGCT
CAAGACATCTATGAAGTTTGTCAAGAATGTGATAGCAGGGATTAGGGAAACTGAAGAGAAAT
TCTACTACATCGTGCAGGAAGAGAAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGG
GGTGGAATGCTAGCCATGCCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGC
CAAGAGTGGCTTCTTTCGGGTGTTTATTGGCGTGAATGACCTTGAAAGGGAGGGACAGTACA
TGTCCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGCGAC
CCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTG
CCATCTTACCATGTACTTTGTCTGTGAGTTCATCAAGAAGAAAAAGTAACTTCCCTCATCCT
ACGTATTTGCTATTTTCCTGTGACCGTCATTACAGTTATTGTTATCCATCCTTTTTTTCCTG
ATTGTACTACATTTGATCTGAGTCAACATAGCTAGAAAATGCTAAACTGAGGTATGGAGCCT
CCATCATCAAAAAAAAAAAAAAAAAA

FIGURE 37

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50980

><subunit 1 of 1, 277 aa, 1 stop

><MW: 30645, pI: 7.47, NX(S/T): 2

MNGFASLLRRNQFILLVLFLLQIQSLGLDIDSRPTAEVCATHHTISPGPKGDDGEKGDGPGEEG
KHGKVGRMGPKGIKGELGDMGDQGNIGKTGPIGKKGDKGEKGLLGIPGEKKGAGTVCDGCRY
RKFBVGQLDISIARLKTSMKFVKNVIAIGIRETEEFYIIVQEEKNYRESLTHCRIRGGMLAMP
KDEAANTLIADYVAKSGFFRVFIGVNDLEREGQYMSTDNTPLQNYSNWNEGEPSDPYGHEDC
VEMLSSGRWNDTECHLTMYFVCEFIKKKK

Signal peptide:

amino acids 1-25

0978187-1050

FIGURE 38

GGTTCTATCGATTCTGAATTCGGCCACACTGGCCGGATCCTCTAGAGATCCCTCGACCTCGAC
 CCACGCGTCCGCTGCTCTCCGCCCGTGTGGAGTGGTGGGGCCCTGGGTGGGAATGGGCGTGT
 GCCAGCGCACGCGCTCCCTGGAAGGAGAAGTCTCAGCTAGAACGAGCGGCCCTAGGTTTT
 CGGAAGGGAGGATCAGGGATGTTTGCAGAGCGGCTGGAACCAGACGGTGCCGATAGAGGAAGC
 GGGCTCCATGGCTGCCCTCCTGCTGCTGCCCCCTGCTGCTGTTGCTACCGCTGCTGCTGCTGA
 AGCTACACCTCTGGCCGCGAGTTGCGCTGGCTTCCGGCGGACTTGGCCTTTGCGGTGCGAGCT
 CTGTGCTGCAAAAGGGCTCTTCGAGCTCGCGCCCTGGCCGCGGCTGCCGCCGACCCGGAAGG
 TCCCGAGGGGGGCTGCAGCCTGGCCTGGCGCCTCGCGGAACCTGGCCCAGCAGCGCGCCGCGC
 ACACCTTTCTCATTACCGGCTCGCGGCGCTTTAGCTACTCAGAGGCGGAGCGCGAGAGTAAC
 AGGGCTGCACGCGCCTTCTACGTGCGCTAGGCTGGGACTGGGGACCCGACGGCGGCGACAG
 CGGCGAGGGGAGCGCTGGAGAAGGCGAGCGGGCAGCGCCGGGAGCCGGAGATGCAGCGGCCG
 GAAGCGGCGCGGAGTTTGCCGGAGGGGACGGTGCCGCCAGAGGTGGAGGAGCCGCCGCCCT
 CTGTACCTGGAGCAACTGTGGCGCTGCTCCTCCCCGCTGGCCCAGAGTTTCTGTGGCTCTG
 GTTCGGGCTGGCCAAGGCCGGCCTGCGCACTGCCTTTGTGCCACCGCCCTGCGCCGGGGCC
 CCCTGCTGCACTGCCTCCGCGAGCTGCGGCGCGCGCGCGCTGGTGCTGGCGCCAGAGTTTCTG
 GAGTCCCTGGAGCCGGACCTGCCCGCCCTGAGAGCCATGGGGCTCCACCTGTGGGCTGCAGG
 CCCAGGAACCCACCTGCTGGAATTAGCGATTTGCTGGCTGAAGTGTCCGCTGAAGTGGATG
 GGCCAGTGCCAGGATACCTCTCTTCCCCCAGAGCATAACAGACACGTGCCTGTACATCTTC
 ACCTCTGGCACCACGGGCCTCCCCAAGGCTGCTCGGATCAGTCATCTGAAGATCCTGCAATG
 CCAGGGCTTCTATCAGCTGTGTGGTGTCCACCAGGAAGATGTGATCTACCTCGCCCTCCCAC
 TCTACCACATGTCCGGTTCCTGCTGGGCATCGTGGGCTGCATGGGCATTGGGGCCACAGTG
 GTGCTGAAATCCAAGTTCTCGGCTGGTCAGTTCTGGGAAGATTGCCAGCAGCACAGGGTGAC
 GGTGTTCCAGTACATTGGGGAGCTGTGCCGATACCTTGTCAACCAGCCCCGAGCAAGGCAG
 AACGTGGCCATAAGGTCCGGCTGGCAGTGGGCAGCGGGCTGCGCCAGATACCTGGGAGCGT
 TTTGTGCGGCGCTTCGGGCCCTGCAGGTGCTGGAGACATATGGACTGACAGAGGGCAACGT
 GGCCACCATCAACTACACAGGACAGCGGGGCGCTGTGGGGCGTGCTTCTGGCTTTACAAGC
 ATATCTTCCCCTTCTCCTTGATTGCTATGATGTCAACACAGGAGAGCCAATTCGGGACCCC
 CAGGGGCACTGTATGGCCACATCTCCAGGTGAGCCAGGGCTGCTGGTGGCCCCGGTAAGCCA
 GCAGTCCCCATTCTGGGCTATGCTGGCGGGCCAGAGCTGGCCCAGGGGAAGTTGCTAAAGG
 ATGTCTTCCGGCCTGGGGATGTTTTCTTCAACACTGGGGACCTGCTGGTCTGCGATGACCAA
 GGTTTTCTCCGCTTCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGGAGAATGTGGC
 CACAACCGAGGTGGCAGAGGTCTTCGAGGCCCTAGATTTTCTTCAGGAGGTGAACGTCTATG
 GAGTCACTGTGCCAGGGCATGAAGGCAGGGCTGGAATGGCAGCCCTAGTTCTGCGTCCCCC
 CACGCTTTGGACCTTATGCAGCTCTACACCCACGTGTCTGAGAACTTGCCACCTTATGCCCG
 GCCCGATTCTCAGGCTCCAGGAGTCTTTGGCCACCACAGAGACCTTCAAACAGCAGAAAG
 TTCGGATGGCAAATGAGGGCTTCGACCCACAGACCCTGTCTGACCACTGTACGTTCTGGAC
 CAGGCTGTAGGTGCCTACCTGCCCCCTCAAACTGCCCGGTACAGCGCCCTCCTGGCAGGAAA
 CCTTCGAATCTGAGAACTTCCACACCTGAGGCACCTGAGAGAGGAACTCTGTGGGGTGGGGG
 CCGTTGCAGGTGTACTGGGCTGTGAGGATCTTTTCTATACCAGAACTGCGGTCACTATTTT
 GTAATAAATGTGGCTGGAGCTGATCCAGCTGTCTCTGACCTAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGTAGGGATAACAGGGTAATAAGC
 TTGGCCGCCATGGCCCAACTTGTTTATTGCAG

FIGURE 39

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50913

><subunit 1 of 1, 730 aa, 1 stop

><MW: 78644, pI: 7.65, NX(S/T): 2

MGVCQRTAPWKEKSQLERAALGFRKGGSGMFASGWNQTVPIEEAGSMAALLLLPLLLLLLPL
LLLKLHLWPQLRWLPADLAFVRLCCKRALRARALAAAADPEGPEGGCSLAWRLAELAQQ
RAAHTFLIHGSRRFSYSEAERESNRAARAFLRALGWDWGPDGGDSGEGSAGEGERAAPGAGD
AAAGSGAEFAGGDGAARGGGAAAPLSPGATVALLLPAGPEFLWLWFGGLAKAGLRTAFVPTAL
RRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEVSA
EVDGPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKILQCQGFYQLCGVHQEDVIYL
ALPLYHMSGSLLGIVGCMGIGATVVLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPP
SKAERGHKVR LAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINYTGQRGAVGRASW
LYKHIFPFSLIRYDVTTGEPIRDPPQGHCMATSPGEPGLLVAPVSQQSPFLGYAGGPPELAQ GK
LLKDVFVRPGDVFFNTGDLVLCDDQGF LRFH DRTGDTFRWKGENVATTEVAEVFEALDFLQEV
NVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPYPYARPRFLRLQESLATTETFK
QQKVRMANEGFDPSTLS DPLYVLDQAVGAYLPLTTARYSALLAGNLRI

Type II transmembrane domain:

amino acids 45-65

Other transmembrane domain:

amino acids 379-398

cAMP- and cGMP-dependent protein kinase phosphorylation site
starting at amino acid 136

CUB domain protein motif

amino acids 254-261

putative AMP-binding domain signature

amino acids 332-343

N-glycosylation sites

amino acids 37-40 and 483-486

09978187-101501

FIGURE 40

CCTGTGTTAAGCTGAGGTTTCCCCTAGATCTCGTATATCCCCAACACATACCTCCACGCACA
CACATCCCCAAGAACCTCGAGCTCACACCAACAGACACACGCGCGCATACACACTCGCTCTC
GCTTGTCCATCTCCCTCCCGGGGGAGCCGGCGCGCGCTCCCACCTTTGCCGCACACTCCGGC
GAGCCGAGCCCGCAGCGCTCCAGGATTCTGCGGCTCGGAACTCGGATTGCAGCTCTGAACCC
CCATGGTGGTTTTTTTAAACACTTCTTTTCCTTCTCTTCCTCGTTTTTGATTGCACCGTTTTCCA
TCTGGGGGCTAGAGGAGCAAGGCAGCAGCCTTCCCAGCCAGCCCTTGTTGGCTTGCCATCGT
CCATCTGGCTTATAAAAAGTTTGCTGAGCGCAGTCCAGAGGGCTGCGCTGCTCGTCCCCTCGG
CTGGCAGAAGGGGGTGACGCTGGGCAGCGGCGAGGAGCGCGCCGCTGCCTCTGGCGGGGCTTT
CGGCTTGAGGGGCAAGGTGAAGAGCGCACCGGCCGTGGGGTTTACCGAGCTGGATTGTATG
TTGCACCAATGCCTTCTTGATCGGGGCTGTGATTCTTCCCCTCTTGGGGCTGCTGCTCTCCC
TCCCCGCCGGGGCGGATGTGAAGGCTCGGAGCTGCGGAGAGGTCCGCCAGGCGTACGGTGCC
AAGGGATTGAGCCTGGCGGACATCCCCTACCAGGAGATCGCAGGGGAACACTTAAGAATCTG
TCCTCAGGAATATACATGCTGCACCACAGAAATGGAAGACAAGTTAAGCCAACAAAGCAAAC
TCGAATTTGAAAACCTTGTGGAAGAGACAAGCCATTTTGTGCGCACCACCTTTTGTGTCCAGG
CATAAGAAATTTGACGAATTTTTCCGAGAGCTCCTGGAGAATGCAGAAAAGTCACTAAATGA
TATGTTTGTACGGACCTATGGCATGCTGTACATGCAGAATTCAGAAGTCTTCCAGGACCTCT
TCACAGAGCTGAAAAGGTACTACACTGGGGGTAAATGTGAATCTGGAGGAAATGCTCAATGAC
TTTTGGGCTCGGCTCCTGGAACGGATGTTTCAGCTGATAAACCCCTCAGTATCACTTCAGTGA
AGACTACCTGGAATGTGTGAGCAAATACACTGACCAGCTCAAGCCATTTGGAGACGTGCCCC
GGAACTGAAGATTGAGTTACCCGCGCCTTCATTGCTGCCAGGACCTTTGTCCAGGGGCTG
ACTGTGGGCAGAGAAGTTGCAAACCGAGTTTCCAAGGTCAGCCCAACCCAGGGTGTATCCG
TGCCCTCATGAAGATGCTGTACTGCCCATACTGTCGGGGGCTTCCCCTGTGAGGCCCTGCA
ACAATACTGTCTCAACGTCATGAAGGGCTGCTTGGCAAATCAGGCTGACCTCGACACAGAG
TGGAATCTGTTTATAGATGCAATGCTCTTGGTGGCAGAGCGACTGGAGGGGGCCATTCAACAT
TGAGTCGGTCATGGACCCGATAGATGTCAAGATTTCTGAAGCCATTATGAACATGCAAGAAA
ACAGCATGCAGGTGTCTGCAAAGGTCTTTCAGGGATGTGGTCAGCCCAACCTGCTCCAGCC
CTCAGATCTGCCCCGCTCAGCTCCTGAAAATTTTAATACAGTTTTCAGGCCCTACAATCCTGA
GGAAAGACCAACAACCTGCTGCAGGCACAAGCTTGGACCGGCTGGTCACAGACATAAAAGAGA
AATTGAAGCTCTCTAAAAAGGTCTGGTCAGCATTACCTTACACTATCTGCAAGGACGAGAGC
GTGACAGCGGGCACGTCCAACGAGGAGGAATGCTGGAACGGGCACAGCAAAGCCAGATACTT
GCCTGAGATCATGAATGATGGGCTCACCAACCAGATCAACAATCCCGAGGTGGATGTGGACA
TCACTCGGCCTGACACTTTCATCAGACAGCAGATTATGGCTCTCCGTGTGATGACCAACAAA
CTAAAAAACGCCTACAATGGCAATGATGTCAATTTCCAGGACACAAGTGATGAATCCAGTGG
CTCAGGGAGTGGCAGTGGGTGCATGGATGACGTGTGTCCACGGAGTTTGAGTTTGTACCA
CAGAGGCCCCCGCAGTGGATCCCGACCGGAGAGAGGTGGACTCTTCTGCAGCCCAGCGTGGC
CACTCCCTGCTCTCCTGGTCTCTCACCTGCATTGTCTTGGCACTGCAGAGACTGTGCAGATA
ATCTTGGGTTTTTGGTCAGATGAACTGCATTTTAGCTATCTGAATGGCCAACCTCACTTCTT
TTCTTACACTCTTGGACAATGGACCATGCCACAAAACTTACCGTTTTCTATGAGAAGAGAG
CAGTAATGCAATCTGCCTCCCTTTTTGTTTTCCCAAAGAGTACCGGGTGCCAGACTGAACTG
CTTCTCTTTCTTTCAGCTATCTGTGGGGACCTTGTTTATTCTAGAGAGAATTCTTACTCAA
ATTTTTCGTACCAGGAGATTTTCTTACCTTCATTGTCTTTATGCTGCAGAAGTAAAGGAAT
CTCACGTTGTGAGGGTTTTTTTTTTCTCATTAAAAAT

FIGURE 41

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50914

><subunit 1 of 1, 555 aa, 1 stop

><MW: 62736, pI: 5.36, NX(S/T): 0

MPSWIGAVILPLLGLLLSLPAGADVKARSCGEVRQAYGAKGFSLADIPYQEIAGEHLRICPQ
EYTCCTTEMEDKLSQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFFRELLENAEKS LNDMF
VRTYGMLYMQNSEVFQDLFTTELKRYYTGGNVNLEEMLNDFWARLLERMFQLINPQYHFSEDY
LECVSKYTDQLKPFQDVPRKLKIQVTRAFIAARTFVQGLTVGREVANRVSKVSPTPGCIRAL
MKMLYCPYCRGLPTVRPCNNYCLNVMKGCLANQADLDTEWNLFIDAMLLVAERLEGPFNIES
VMDPIDVKISEAIMNMQENSMQVSAKVFQGGQPKPAPALRSARSAPENFNTRFRPYNPEER
PTTAAGTSLDRLVTDIKEKLKLSKKVWSALPYTICKDESVTAGTSNEEECWNGHISKARYLPE
IMNDGLTNQINNPEVDVDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESSGSG
SGSGCMDDVCPTEFEFVTTEAPAVDPDRREVDSSAAQRGHSLLSWSLTCIVLALQRLCR

Signal peptide:

amino acids 1-23

09978187-101501
TOSTOT-2818/660

FIGURE 42A

CGGACGCGTGGGCGGACGCGTGGGCAAAAGAACTCGGAGTGCCAAAGCTAAATAAGTTAGCTGAGAAAACGCACG
CAGTTTGCAGCGCCTGCGCCGGGTGCGCCAACTACGCAAAGACCAAGCGGGCTCCGCGCGGACCGGCCGCGGGG
TAGGGACCCGGCTTTGGCCTTCAGGCTCCCTAGCAGCGGGGAAAAGGAATTGCTGCCCGGAGTTTCTGCGGAGGT
GGAGGGAGATCAGGAAACGGCTTCTTCCTCACTTCGCCCGCTGGTGAGTGTGCGGGAGATTGGCAAACGCCTAGG
AAAGGACTGGGGAAAATAGCCCTGGGAAAGTGGAGAAGGTGATCAGGAGGCCGGTCCACTACGGCAGTTTATCTG
TCTGATCAGAGCCAGACGCGACGCGTCCACTTCGCAGTTCTTTCCAGGTGTGGGGACCGCAGGACAGACGGCCGA
TCCCCGCCCCCTCCGTACCAGCACTCCAGGAGAGTCAGCCTCGCTCCCCAACGTCGAGGGCGCTCTGGCCACGA
AAAGTTCCTGTCCACTGTGATTCTCAATTCTTGCTTGGTTTTTTTCTCCAGAGAACTTTTGGGTGGAGATATTA
ACTTTTTTCTTTTTTTTTTCTTGCTTGGTGAAGCTGCTCTAGGGAGGGGGAGGAGGAGGAGAAAGTGAAATGTGC
TGGAGAAGAGCGAGCCCTCCTTGTTCTTCCGGAGTCCCATCCATTAAGCCATCACTTCTGGAAGATTAAAGTTGT
CGGACATGGTGACAGCTGAGAGGAGAGGAGGATTTCTTGCCAGGTGGAGAGTCTTCACCGTCTGTTGGGTGCATG
TGTGCGCCCCGACGCGCGCGGGGCGCGTGGTTCTCCGCGTGAGTCTCACCTGGGACCTGAGTGAATGGCTCCCA
GGGGCTGTGCGGGGCATCCGCCTCCGCCTTCTCCACAGGCCTGTGTCTGTCTGCTGGAAAGATGCTAGCAATGGGGG
CGCTGGCAGGATTCTGGATCCTCTGCCTCCTCACTTATGGTTACCTGTCTGCTGGGGCCAGGCCCTTAGAAGAGGAGG
AAGAAGGGGCCTTACTAGCTCAAGCTGGAGAGAACTAGAGCCAGCACAACCTCCACCTCCCAGCCCCATCTCA
TTTTCATCCTAGCGGATGATCAGGGATTTAGAGATGTGGGTACCACGGATCTGAGATTAAACACCTACTCTTG
ACAAGCTCGCTGCCGAAGGAGTTAAACTGGAGAACTACTATGTCCAGCCTATTTGCACACCATCCAGGAGTCAGT
TTATTACTGGAAGTATCAGATACACACCGGACTTCAACATTCTATCATAAGACCTACCCAACCCAAGTGTTTAC
CTCTGGACAATGCCACCTACCTCAGAACTGAAGGAGGTTGGATATTCAACGCATATGGTTCGGAAAATGGCACT
TGGGTTTTAACAGAAAAGATGCATGCCACCCAGAAGAGGATTTGATACCTTTTTTGGTTCCCTTTTGGGAAGTG
GGGATTACTATACACTACAAATGTGACAGTCTTGGGATGTGTGGCTATGACTTGTATGAAAACGACAATGCTG
CCTGGGACTATGACAATGGCATATACTCCACACAGATGTACACTCAGAGAGTACAGCAAATCTTAGCTTCCATA
ACCCCAAAAGCCTATATTTTTATATACTGCCTATCAAGCTGTTTCATTACCACTGCAAGCTCCTGGCAGGTATT
TCGAACACTACCGATCCATTATCAACATAAACAGGAGAAGATATGCTGCCATGCTTTCTGCTTAGATGAAGCAA
TCAACAACGTGACATTGGCTCTAAAGACTTATGGTTTCTATAACAACAGCATTATCATTTACTCTTCAGATAATG
GTGGCCAGCCTACGGCAGGAGGGAGTAAGTGGCCTCTCAGAGGTAGCAAAGGAACATATTGGGAAGGAGGGATCC
GGGCTGTAGGCTTTGTGCATAGCCCACTTCTGAAAAACAAGGGAACAGTGTGTAAGGAACTTGTGCACATCACTG
ACTGGTACCCCACTCTCATTTCACTGGCTGAAGGACAGATTGATGAGGACATTCAACTAGATGGCTATGATATCT
GGGAGACCATAAGTGAGGGTCTTCGCTCACCCCGAGTAGATATTTGCATAACATTGACCCCTATACACCAAGGC
AAAAAATGGCTCCTGGGCAGCAGGCTATGGGATCTGGAACACTGCAATCCAGTCAGCCATCAGAGTGCAGCACTG
GAAATTGCTTACAGGAAATCCTGGCTACAGCGACTGGGTCCCCCTCAGTCTTTCAGCAACCTGGGACCGAACC
GTGGCACAATGAACGGATCACCTTGTCAACTGGCAAAAGTGTATGGCTTTTCAACATCACAGCCGACCCATATGA
GAGGGTGGACCTATCTAACAGGTATCCAGGAATCGTGAAGAAGCTCCTACGGAGGCTCTCACAGTTCAACAAAAC
TGCAGTGCCGGTCAGGTATCCCCCAAAGACCCCAAGTAACCTAGGCTCAATGGAGGGGTCTGGGGACCATG
GTATAAAGAGGAAACCAAGAAAAAGCAAGCAAAATCAGGCTGAGAAAAAGCAAAAGAAAAGCAAAAAA
GAAGAAGAAACAGCAGAAAGCAGTCTCAGGTAAACCAGCAAATTTGGCTCGATAATATCGCTGGCCTAAGCGTCA
GGCTTGTTTTTCTGCTGTGCCACTCCAGAGACTTCTGCCACCTGGCCGCCCACTGAAAAGTGTCTGCTCAGTG
CCAAGGTGCTACTCTTGCAAGCCACACTTAGAGAGAGTGGAGATGTTTATTTCTCTCGCTCCTTTAGAAAACGTG
GTGAGTCTTGAGTTCCACTGCTGTGCTTCAGTCAACTGACCAAACACTGCTTTGAATTATAGGAGGAGAACAATA
ACCTACCATCCGCAAGCATGCTAATTTGATGGAAGTTACAGGGTAGCATGATTAAGAACTACCTTTGATAAATTAC

FIGURE 42B

AGTCAAAGATTGTGTCACCTCAAAGGCCTTGAAGAATATATTTTCTTGGTGAATTTTTGTATGTCTGT CATATGA
CACTTGGGTTTTTTAATTAATTCATTTTTATATATATAAATATATGTTTCTTTTCCTGTGAAAAGCTGTTTTTCT
CACATGTGAACAGCTTGCACCTCATTTTACCATGCGTGAGGGAATGGCAAATAAGAATGTTTGAGCACACTGCCC
ACAATGAATGTAAC TATTTTCTAAACACTTTACTAGAAGAACATTT CAGTATAAAAAACCTAATTTATTTTACA
GAAAAATATTTTGTGTGTTTTTATAAAAAGTTATGCAAATGACTTTTATTTTATTTTCTGCATACCATTAGAAGA
ATTTTATTTTCATTTCTTCAAATTATCAAGCACTGTAATACTATAAATTAATGTAATACTGTGTGAATTCAGACTA
TAAAAAACATCATTCAGAAAAC TTTATAATCGTCATTGTTCAATCAAGATTTTGAATGTAATAAGATGAATATAT
ATTACTTGGAAATTC AATGTTTGTGCAGAGTTGAGACAACTTTATTTGTTTCTATCATAAACTATTTATGTATCTT
AATTATTAAAAATGATTTACTTTTATGGCACTAGAAAATTTACTGTGGCTTTTCTGTATCTAACTTCTAGCTAAAATT
GTATCATTTGGTCCTAAAAAATAAAAAATCTTTACTAATAGGCAATTGAAGGAATGGTTTGCTAACAACCACAGTAA
TATAATATGATTTTACAGATAGATGCTTCCCCTGGCTATGACATGGAGAAAAGATTTTCCCATATAATAAATACTAA
TATTTATATTAGGTTGGTGCAAAACTAGTTGCGGTTTTTCCCATTA AAAAGTAATAACCTTACTCTTATACAAAGT
GGACACTGTGGGGAGATACAGAGAAATGGAAGATACGGATCCTGCCTGGAGTAGGTAACCTTGCTTGGAACCCCC
ACATGCAAACGTCATGAGGAGAATTAAAGGAGTATTATCAGTAATGAAGTTTATCATGGGTCATCAATGAGCATA
GATTGGTGTGGATCCTGTAGACCCCTGGTGTTTTTCTTTGAAGTGCCCTCTCCTAATGCAGAGGCCCTTGAAGCTTAC
AGTATACACTTGAAAAGTCACAGATAGCTAGAATTATGATCTTTGAAGTTATAACTGTGATCTGAAAATGTGTGT
GGTGGTATGACAGCATACCATTAAATACATTTACATCACAGCTCAAAGGACTGTGATATAATCCATTTATATCAC
AACTCAAAGGACTGTGATATAATCCATTTATATCACAGCTCACAGTTTCTGAAAATGTATAAAAGAATCTATAAT
CTAGTACTGAAATTACTAAATTTGGGTAAGATGATTTAAATGATTTTAATTTTAACATTTTATTTCTAGAATATAT
GGCTCCATTTTATTTTATAGTGTAAGTTGTATTTCTAAAGTTTGTGTTTGTGCGACAGTATCTTTTAAATGAG
TCTTAAAAATAAAGGCATATTGTTTCATGTTTAAA
AAA

05978187-101501

FIGURE 43

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48296

><subunit 1 of 1, 515 aa, 1 stop

><MW: 56885, pI: 6.49, NX(S/T): 5

MAPRGCAGHPPPPSPQACVCPGKMLAMGALAGFWILCLLTGYLSWGQALEEEEEEGALLAQA
GEKLEPSTTSTSQPHLIFILADDQGFRDVGYPHYGSEIKTPTLDKLAAGVKLENYYVQPICTP
SRSQFITGKYQIHTGLQHSIIRPTQPNCLPLDNATLPQKLKEVGYSTHMGVKGWHLGFNRKEC
MPTRRGFDTFFGSLLGSGDYTHYKCDSPGMCYDLYENDNAAWDYDNGIYSTQMYTQRVQQ
ILASHNPTKPIFLYTAYQAVHSPLQAPGRYFEHYRSIININRRRYAAMLSCLEAINNVTLA
LKTYGFYNNNSIIYSSDNGGQPTAGGSNWPLRGSKGTYWEGGIRAVGVHSPLLKNKGTVC
ELVHITDWYPTLISLAEGQIDEDIQLDGYDIWETISEGLRSPRVDILHNIDPYTPRQKMAPG
QQAMGSGTLQSSQPSECSTGNCLQEILATATGSPLSLSATWDRTGGTMNGSPCQLAKVYGF
TSQPTHMRGWTYLTGIQES

Important Features:

Signal Peptide:

amino acids 1-37

Sulfatases signature 1.

amino acids 120-132

Sulfatases signature 2.

amino acids 168-177

Tyrosine kinase phosphorylation site.

amino acids 163-169

N-glycosylation sites.

amino acids 157-160, 306-309 and 318-321

09978187-101501

FIGURE 44

CGGACGCGTGGGTGCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGAGAGAGGAGGCGGCGGC
TTAGCTGCTACGGGGTCCGGCCGGCGCCCTCCCGAGGGGGGCTCAGGAGGAGGAAGGAGGAC
CCGTGCGAGAATGCCTCTGCCCTGGAGCCTTGCGCTCCCGCTGCTGCTCTCCTGGGTGGCAG
GTGGTTTTCGGGAACGCGGCCAGTGCAAGGCATCACGGGTTGTTAGCATCGGCACGTCAGCCT
GGGGTCTGTCACTATGGAACCTAACTGGCCTGCTGCTACGGCTGGAGAAGAAACAGCAAGGG
AGTCTGTGAAGCTACATGCGAACCTGGATGTAAGTTTGGTGAAGTGGTGGGACCAAACAAAT
GCAGATGCTTTCCAGGATACACCGGGAAAACCTGCAGTCAAGATGTGAATGAGTGTGGAATG
AAACCCCGGCCATGCCAACACAGATGTGTGAATACACACGGAAGCTACAAGTGCTTTTGCCT
CAGTGGCCACATGCTCATGCCAGATGCTACGTGTGTGAACCTCTAGGACATGTGCCATGATAA
ACTGTCAGTACAGCTGTGAAGACACAGAAGAAGGGCCACAGTGCCTGTGTCCATCCTCAGGA
CTCCGCTGGCCCCAAATGGAAGAGACTGTCTAGATATTGATGAATGTGCCTCTGGTAAAGT
CATCTGTCCCTACAATCGAAGATGTGTGAACACATTTGGAAGCTACTACTGCAAATGTCACA
TTGGTTTTCGAACTGCAATATATCAGTGGACGATATGACTGTATAGATATAAATGAATGTACT
ATGGATAGCCATACGTGCAGCCACCATGCCAATTGCTTCAATACCCAAGGGTCCTTCAAGTG
TAAATGCAAGCAGGGATATAAAGGCAATGGACTTCGGTGTCTGCTATCCCTGAAAATTCTG
TGAAGGAAGTCCTCAGAGCACCTGGTACCATCAAAGACAGAATCAAGAAGTTGCTTGCTCAC
AAAAACAGCATGAAAAAGAAGGCAAAAATTAAAAATGTTACCCCAAGCCACCAGGACTCC
TACCCCTAAGGTGAACTTGCAGCCCTTCAACTATGAAGAGATAGTTTCCAGAGGCGGGAAC
CTCATGGAGGTAAAAAAGGGAATGAAGAGAAATGAAGAGGGGCTTGAGGATGAGAAAAGAG
AAGAGAAAGCCCTGAAGAATGACATAGAGGAGCGAAGCCTGCGAGGAGATGTGTTTTTCCCT
AAGGTGAATGAAGCAGGTGAATTCGGCCTGATTCTGGTCCAAAGGAAAGCGCTAACTTCCAA
ACTGGAACATAAAGATTTAAATATCTCGGTTGACTGCAGCTTCAATCATGGGATCTGTGACT
GGAAACAGGATAGAGAAGATGATTTTGACTGGAATCCTGCTGATCGAGATAATGCTATTGGC
TTCTATATGGCAGTTCCGGCCTTGGCAGGTCAAGAAAGACATTGGCCGATTGAACTTCT
CCTACCTGACCTGCAACCCCAAAGCAACTTCTGTTTGCTCTTTGATTACCGGCTGGCCGGAG
ACAAAGTCGGGAAACTTCGAGTGTGTTGTGAAAAACAGTAACAATGCCCTGGCATGGGAGAAG
ACCACGAGTGAGGATGAAAAGTGGAAGACAGGGAAAATTGAGTTGTATCAAGGAACTGATGC
TACCAAAGCATCATTTTTGAAGCAGAACGTGGCAAGGGCAAACCGGCGAAATCGCAGTGG
ATGGCGTCTTGCTTGTTTCAGGCTTATGTCCAGATAGCCTTTTATCTGTGGATGACTGAATG
TTACTATCTTTATATTTGACTTTGTATGTCAGTTCCTGGTTTTTTTGATATTGCATCATAG
GACCTCTGGCATTTTAGAACTTAGCTGAAAAATTGTAATGTACCAACAGAAATATTATTG
TAAGATGCCTTTCTTGATAAGATATGCCAATATTTGCTTTAAATATCATATCACTGTATCT
TCTCAGTCATTTCTGAATCTTTCNCATTATATTATAAAATNTGGAAANGTCAGTTTATCTC
CCCTCCTCNGTATATCTGATTTGTATANGTANGTTGATGNGCTTCTCTCTACAACATTTCTA
GAAAATAGAAAAAAAAGCACAGAGAAATGTTTAACTGTTTGACTCTTATGATACTTCTTGGA
AACTATGACATCAAAGATAGACTTTTGCCTAAGTGGCTTAGCTGGGTCTTTCATAGCCAAAC
TTGTATATTTAATTCTTTGTAATAATAA

FIGURE 45

MPLPWSLALPLLLSWVAGGFGNAASARHHGLLASARQPGVCHYGTKLACCYGWRNRNSKGVCE
ATCEPGCKFGECVGPNNKRCFPGYTGKTCSQDVNECGMKPRPCQHRVCNTHGSYKCFCLSGH
MLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCPSSGLRLAPNGRDCLDIDECASGKVICP
YNRRCVNTFGSYYCKCHIGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQGSFKCKCK
QGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAHKNSMKKKAKIKNVTPEPTRTPPK
VNLQPFNYEEIVSRGGNSHGGKKGNEEK

Signal peptide:

amino acids 1-21

EGF-like domain cysteine pattern signature.

amino acids 80-91

Calcium-binding EGF-like domains

amino acids 103-124, 230-251 and 185-206

09978187 101501
TOSTOT 28T82660

FIGURE 46

GGGAGCTGCTGCTGTGGCTGCTGGTGCTGTGCGCGCTGCTCCTGCTCTTGGTGCAGCTGCTG
CGCTTCCTGAGGGCTGACGGCGACCTGACGCTACTATGGGCCGAGTGGCAGGGACGACGCCC
AGAATGGGAGCTGACTGATATGGTGGTGTGGGTGACTGGAGCCTCGAGTGGAATTGGTGAGG
AGCTGGCTTACCAGTTGTCTAAACTAGGAGTTTCTCTTGCTGTGCTGTCAGCCAGAAGAGTGCAT
GAGCTGGAAAGGGTGAAAAGAAGATGCCTAGAGAATGGCAATTTAAAAGAAAAAGATATACT
TGTTTTGCCCCCTTGACCTGACCGACACTGGTTCCCATGAAGCGGCTACCAAAGCTGTTCTCC
AGGAGTTTGGTAGAATCGACATTCTGGTCAACAATGGTGGAATGTCCAGCGTTCTCTGTGC
ATGGATAACCAGCTTGGATGTCTACAGAAAGCTAATAGAGCTTAACTACTTAGGGACGGTGTC
CTTGACAAAATGTGTTCTGCCTCACATGATCGAGAGGAAGCAAGGAAAGATTGTTACTGTGA
ATAGCATCCTGGGTATCATATCTGTACCTCTTTCCATTGGATACTGTGCTAGCAAGCATGCT
CTCCGGGGTTTTTTTTAATGGCCTTCGAACAGAACTTGCCACATACCCAGGTATAATAGTTTC
TAACATTTGCCCAGGACCTGTGCAATCAAATATTGTGGAGAATTCCCTAGCTGGAGAAGTCA
CAAAGACTATAGGCAATAATGGAGACCAGTCCCACAAGATGACAACCAGTCGTTGTGTGCGG
CTGATGTTAATCAGCATGGCCAATGATTTGAAAGAAGTTTGGATCTCAGAACAACCTTTCTT
GTTAGTAACATATTTGTGGCAATACATGCCAACCTGGGCCTGGTGGATAACCAACAAGATGG
GGAAGAAAAGGATTGAGAACTTTAAGAGTGGTGTGGATGCAGACTCTTCTTATTTTAAAATC
TTTAAGACAAAACATTGACTGAAAAGAGCACCTGTACTTTTCAAGCCACTGGAGGGAGAAATG
GAAAACATGAAAACAGCAATCTTCTTATGCTTCTGAATAATCAAAGACTAATTTGTGATTTT
ACTTTTTAATAGATATGACTTTGCTTCCAACATGGAATGAAATAAAAAATAATAATAAAAG
ATTGCCATGAATCTTGCAAAA

0978197-101501

FIGURE 47

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA36343

><subunit 1 of 1, 289 aa, 1 stop

><MW: 32268, pI: 9.21, NX(S/T): 0

MVVWVTGASSGIGEELAYQLSKLGVSLVLSARRVHELERVKRRCLENGNLKEKDILVLPDL
TDTGSHEAATKAVLQEFGRIDILVNNGGMSQRSCLMDTSLDVYRKLIELNYLGTVSLTKCVL
PHMIERKQGKIVTVNSILGIISVPLSIGYCASKHALRGFFNGLRTELATYPGIIIVSNICPGP
VQSNIVENSLAGEVTKTIGNNGDQSHKMTT SRCVRLMLISMANDLKEVWISEQPFLLVTYLW
QYMPTWAWWITNKMGGKKRIENFKSGVDADSSYFKIFKTKHD

Important Features:

Signal Peptide:

amino acids 1-31

Transmembrane domain:

amino acids 136-157

Tyrosine kinase phosphorylation site.

106-113 and 107-114

Homologous region to Short-chain alcohol dehydrogenase

amino acids 80-90, 131-168, 1-13 and 176-185

09078187-101501

FIGURE 48

GCGACGTGGGCACCGCCATCAGCTGTTTCGCGCGTCTTCTCCTCCAGGTGGGGCAGGGGTTTC
GGGCTGGTGGAGCATGTGCTGGGACAGGACAGCATCCTCAATCAATCCAACAGCATATTTCGG
TTGCATCTTCTACACACTACAGCTATTGTTAGGTTGCCTGCGGACACGCTGGGCCTCTGTCC
TGATGCTGCTGAGCTCCCTGGTGTCTCTCGCTGGTTCTGTCTACCTGGCCTGGATCCTGTTC
TTCGTGCTCTATGATTTCTGCATTGTTTGTATCACCACCTATGCTATCAACGTGAGCCTGAT
GTGGCTCAGTTTCCGGAAGGTCCAAGAACCCAGGGCAAGGCTAAGAGGCACTGAGCCCTCA
ACCCAAGCCAGGCTGACCTCATCTGCTTTGCTTTGGTCTTCAAGCCGCTCAGCGTGCCTGTG
GACAGCGTGGCCCCGGCCCCCCCCAAGCCTCAGGAGGGCAACACAGTCCCTGGCGAGTGGCCC
TGGCAGGCCAGTGTGAGGAGGCAAGGAGCCCACATCTGCAGCGGCTCCCTGGTGGCAGACAC
CTGGGTCTTCACTGCTGCCCCACTGCTTTGAAAAGGCAGCAGCAACAGAAGTGAATTCCTGGT
CAGTGGTCTTGGGTTCTCTGCAGCGTGAGGGACTCAGCCCTGGGGCCGAAGAGGTGGGGGTG
GCTGCCCTGCAGTTGCCCAGGGCCTATAACCACTACAGCCAGGGCTCAGACCTGGCCCTGCT
GCAGCTCGCCACCCACGACCCACACACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCC
CCTTTGGAGCCTCCTGCTGGGCCACTGGCTGGGATCAGGACACCAGTGATGCTCCTGGGACC
CTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAACTGTATCTACAACCAGCT
GCACCAGCGACACCTGTCCAACCCGGCCCCGGCCTGGGATGCTATGTGGGGGCCCCCAGCCTG
GGGTGCAGGGCCCCCTGTGAGGGAGATTCCGGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGA
CACTGGGTTTCAAGCTGGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGGACGCTCCTGT
GCTGCTGACCAACACAGCTGCTCACAGTTCCTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTT
TCCTGGCCCAGAGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGA
TCCTTGAGGACAGCAGGTCCCCAGGCAGGAGACCCCTCCCCATGGCCCTGGGAGGCCAGGCT
GATGCACCAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGGCGGTGCTAACTG
CTGCCCACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGA
CCGGAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCTGAGGGGGG
CTACGACATGGCCCTCCTGCTGCTGGCCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCCC
TCTGCCTGCCCTATCCTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTTCTGGGACGG
GCCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCTCCTGGGGCCTAG
GGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCGGGGATGG
TGTGTACCAAGTGCTGTGGGTGAGCTGCCCAGCTGTGAGGGCCTGTCTGGGGCACCCTGGTG
CATGAGGTGAGGGGCACATGGTTTCTGGCCGGGCTGCACAGCTTCGGAGATGCTTGCCAAGG
CCCCGCCAGGCCGGCGGTCTTACC CGCTCCCTGCCTATGAGGACTGGGTGAGCAGTTTGG
ACTGGCAGGTCTACTTCGCCGAGGAACCAAGAGCCCGAGGCTGAGCCTGGAAGCTGCCTGGCC
AACATAAGCCAACCAACCAGCTGCTGACAGGGGACCTGGCCATTCTCAGGACAAGAGAATGC
AGGCAGGCAAATGGCATTACTGCCCCCTGTCTCCCCACCCTGTGATGTGTGATTCCAGGCAC
CAGGGCAGGCCCAGAAGCCCAGCAGCTGTGGGAAGGAACCTGCCTGGGGCCACAGGTGCCCA
CTCCCCACCCTGCAGGACAGGGGTGTCTGTGGACACTCCACACCCAACTCTGCTACCAAGC
AGGCGTCTCAGCTTTCCTCCTCTTACTCTTTTTCAGATACAATCACGCCAGCCACGTTGTTT
TGAAAATTTCTTTTTTTTGGGGGGCAGCAGTTTTCTTTTTTTTAACTTAAATAAATTGTTAC
AAAATAAAA

0997818710504

FIGURE 49

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40571

MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGNTV
PGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPGA
EEVGVAALQLPRAYNHYSQGS DLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATGWDQDTS
DAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVLC
LEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSPETPEMSDEDS
CVACGSLRTAGPQAGAPSPWPWEARLMHQQLACGGALVSEEAVLTAAHCFIGRQAPEEWSV
GLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYPDHHLPDGERG
WVLGRARPGAGISSLQTVPVTLTGPRACSR LHAAPGGDGSPILPGMVCTSAVGELPSCEGLS
GAPLVHEVRGTWFLAGLHSFGDACQGPAPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEPE
GSCLANISQPTSC

Important features:

Signal peptide:

amino acids 1-15

Homologous region to Serine proteases, trypsin family

amino acids 79-95, 343-359 and 237-247

N-glycosylation sites.

amino acids 37-40 and 564-567

Kringle domains

amino acids 79-96, 343-360 and 235-247

FIGURE 50

CGGGCCGCCCCCGGCCCCCATTCGGGCGGGCCTCGCTGCGGCGGCGACTGAGCCAGGCTGG
GCCGCGTCCCTGAGTCCCAGAGTCGGCGCGGCGCGGCAGGGGCAGCCTTCCACCACGGGGAG
CCCAGCTGTCAGCCGCCTCACAGGAAGATGCTGCGTCGGCGGGGCAGCCCTGGCATGGGTGT
GCATGTGGGTGCAGCCCTGGGAGCACTGTGGTTCTGCCTCACAGGAGCCCTGGAGGTCCAGG
TCCCTGAAGACCCAGTGGTGGCACTGGTGGGCACCGATGCCACCCTGTGCTGCTCCTTCTCC
CCTGAGCCTGGCTTCAGCCTGGCACAGCTCAACCTCATCTGGCAGCTGACAGATACCAAACA
GCTGGTGCACAGCTTTGCTGAGGGCCAGGACCAGGGCAGCGCCTATGCCAACCGCACGGCCC
TCTTCCCGGACCTGCTGGCACAGGGCAACGCATCCCTGAGGCTGCAGCGCGTGGGTGTGGCG
GACGAGGGCAGCTTCACCTGCTTCGTGAGCATCCGGGATTTCCGCAGCGCTGCCGTACGCCT
GCAGGTGGCCGCTCCCTACTCGAAGCCCAGCATGACCCTGGAGCCCAACAAGGACCTGCGGC
CAGGGGACACGGTGACCATCACGTGCTCCAGCTACCAGGGCTACCCTGAGGCTGAGGTGTTT
TGGCAGGATGGGCAGGGTGTGCCCCCTGACTGGCAACGTGACCACGTGCGAGATGGCCAACGA
GCAGGGCTTGTTTGATGTGCACAGCGTCCTGCGGGTGGTGTGCGGTGCGAATGGCACCTACA
GCTGCCTGGTGCGCAACCCCGTGCTGCAGCAGGATGCGCACRGCTCTGTCAACCATCACAGGG
CAGCCTATGACATTCCCCCAGAGGGCCCTGTGGGTGACCGTGGGGCTGTCTGTCTGTCTCAT
TGCACTGCTGGTGGCCCTGGCTTTTCGTGTGCTGGAGAAAGATCAAACAGAGCTGTGAGGAGG
AGAATGCAGGAGCTGAGGACCAGGATGGGGAGGGAGAAGGCTCCAAGACAGCCCTGCAGCCT
CTGAAACACTCTGACAGCAAAGAAGATGATGGACAAGAAATAGCCTTGACCATGAGGACCAGG
GAGCTGCTACCCCTCCCTACAGCTCCTACCCTCTGGCTGCAATGGGGCTGCACTGTGAGCCC
TGCCCCCAACAGATGCATCCTGCTCTGACAGGTGGGCTCCTTCTCCAAAGGATGCGATACAC
AGACCACTGTGCAGCCTTATTTCTCCAATGGACATGATTCCCAAGTCATCCTGCTGCCTTTT
TTCTTATAGACACAATGAACAGACCACCCACAACCTTAGTTCTCTAAGTCATCCTGCCTGCT
GCCTTATTTACAGTACATACATTTCTTAGGGACACAGTACACTGACCACATCACCACCCTC
TTCTTCCAGTGCTGCGTGGACCATCTGGCTGCCTTTTTTCTCCAAAAGATGCAATATTCAGA
CTGACTGACCCCTGCCTTATTTACCAAAGACACGATGCATAGTACCCCGGCCTTGTTTC
TCCAATGGCCGTGATACACTAGTGATCATGTTTCCAGCCCTGCTTCCACCTGCATAGAATCTTT
TCTTCTCAGACAGGGACAGTGCGGCCTCAACATCTCCTGGAGTCTAGAAGCTGTTTCCTTTC
CCCTCCTTCCCTCCCTGCCCCAAGTGAAGACAGGGCAGGGCCAGGAATGCTTTGGGGACACCG
AGGGGACTGCCCCCACCACCATGGTGCTATTCTGGGGCTGGGGCAGTCTTTTCTGGC
TTGCCTCTGGCCAGCTCCTGGCCTCTGGTAGAGTGAGACTTCAGACGTTCTGATGCCTTCCG
GATGTCATCTCTCCCTGCCCCAGGAATGGAAGATGTGAGGACTTCTAATTTAAATGTGGGAC
TCGGAGGGATTTTGTAACCTGGGGGTATATTTTGGGGAAAATAAATGTCTTTGTAAAAAAA
AAAAAAAAAAAAA

05978187-101501

FIGURE 51

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41386

><subunit 1 of 1, 316 aa, 1 stop, 1 unknown

><MW: -1, pI: 4.62, NX(S/T): 4

MLRRRGSPGMGVHVGAAALGALWFCLTGALEVQVPEDPVVALVGTDATLCCSFSPPEPGFSLAQ
LNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALFPDLLAQGNASLRLQVRVADEGSFTCFV
SIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDVTITCSSYQGYPEAEVFWQDGQGVPL
TGNVTTSQMANEQGLFDVHSLRVVLGANGTYSCLVRNPVLQQDAHXSVTITGQPMTFPPEA
LWVTVGLSVCLIALLLVALAFVCWRKIKQSCEEENAGAEDQDGEGEKSKTALQPLKHSDSKED
DGQEIA

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 251-270

N-glycosylation site.

amino acids 91-94, 104-107, 189-192 and 215-218

Homologous region to Immunoglobulins and MHC

amino acids 217-234

09978187-10501

FIGURE 52

TTCGTGACCCTTGAGAAAAGAGTTGGTGGTAAATGTGCCACGTCTTCTAAGAAGGGGGAGTC
CTGAACTTGTCTGAAGCCCTTGTCCGTAAGCCTTGAAGTACGTTCTTAAATCTATGAAGTCG
AGGGACCTTTTCGTGCTTTTTGTAGGGACTTCTTTCCTTGCTTCAGCAACATGAGGCTTTTCT
TGTGGAACGCGGTCTTGACTCTGTTTCGTCACTTCTTTGATTGGGGCTTTGATCCCTGAACCA
GAAGTGAAAATTGAAGTTCTCCAGAAGCCATTCATCTGCCATCGCAAGACCAAAGGAGGGGA
TTTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAGGACGGCTCCTTATTTCACTCCACTC
ACAAACATAACAATGGTCAGCCCATTTGGTTTACCCTGGGCATCCTGGAGGCTCTCAAAGGT
TGGGACCAGGGCTTGAAAGGAATGTGTGTAGGAGAGAAGAGAAAGCTCATCATTCTCCTGC
TCTGGGCTATGGAAAAGAAGGAAAAGGTAAAATTCCCCCAGAAAGTACACTGATATTTAATA
TTGATCTCCTGGAGATTGCAAATGGACCAAGATCCCATGAATCATTCCAAGAAATGGATCTT
AATGATGACTGGAACTCTCTAAAGATGAGGTTAAAGCATATTTAAAGAAGGAGTTTGAAAA
ACATGGTGCGGTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTTTGATAAAG
AAGATGAAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACACGATGAGTTA
TAGAGATACATCTACCCTTTTAAATATAGCACTCATCTTCAAGAGAGGGCAGTCATCTTTAA
AGAACATTTTATTTTTTATACAATGTTCTTTCTTGCTTTGTTTTTATTTTTTATATATTTTTT
CTGACTCCTATTTAAAGAACCCCTTAGGTTTCTAAGTACCCATTTCTTTCTGATAAGTTATT
GGGAAGAAAAAGCTAATTGGTCTTTGAATAGAAGACTTCTGGACAATTTTTCACTTTCACAG
ATATGAAGCTTTGTTTTACTTTCTCACTTATAAATTTAAATGTTGCAACTGGGAATATAACC
ACGACATGAGACCAGGTTATAGCACAAATTAGCACCCCTATATTTCTGCTTCCCTCTATTTTC
TCCAAGTTAGAGGTCAACATTTGAAAAGCCTTTTGCAATAGCCCAAGGCTTGCTATTTTCAT
GTTATAATGAAATAGTTTATGTGTAAGTGGCTCTGAGTCTCTGCTTGAGGACCAGAGGAAAA
TGGTTGTTGGACCTGACTTGTTAATGGCTACTGCTTTACTAAGGAGATGTGCAATGCTGAAG
TTAGAAACAAGGTTAATAGCCAGGCATGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAG
GCTGAGGCGGGCGGATCACCTGAGGTTGGGAGTTCGAGACCAGCCTGACCAACACGGAGAAA
CCCTATCTCTACTAAAAATACAAAGTAGCCCGGCGTGGTGATGCGTGCCTGTAATCCCAGCT
ACCCAGGAAGGCTGAGGCGGCAGAATCACTTGAACCCGAGGCCGAGGTTGCGGTAAGCCGAG
ATCACCTNCAGCCTGGACACTCTGTCTCGAAAAAAGAAAAGAACACGGTTAATACCATATNA
ATATGTATGCATTGAGACATGCTACCTAGGACTTAAGCTGATGAAGCTTGGCTCCTAGTGAT
TGGTGGCCTATTATGATAAATAGGACAAATCATTTATGTGTGAGTTTCTTTGTAATAAAATG
TATCAATATGTTATAGATGAGGTAGAAAGTTATATTTATATTCAATATTTACTTCTTAAGGC
TAGCGGAATATCCTTCCCTGGTTCTTTAATGGGTAGTCTATAGTATATTATACTACAATAACA
TTGTATCATAAGATAAAGTAGTAAACAGTCTACATTTTCCCATTTCTGTCTCATCAAAAAC
TGAAGTTAGCTGGGTGTGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGGGCCAAGGAGGG
TGGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTCTA
CTAAAAATACAAAAATTAGCCAGGCGTGGTGGTGCACACCTGTAGTCCCAGCTACTCGGGAG
GCTGAGACAGGAGATTTGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCAAGATTGTGCC
ACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCATCTCAAAAAAAAAAAAAAGAAGCAGA
CCTACAGCAGCTACTATTGAATAAATACCTATCCTGGATTTT

09701 " 23134650

FIGURE 53

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44194

><subunit 1 of 1, 211 aa, 1 stop

><MW: 24172, pI: 5.99, NX(S/T): 1

MRLFLWNAVLTLFVTSLIGALIPPEVKIEVLQKPFICHRKTKGGDLMLVHYEGYLEKDGSL
FHSTHKHNNNGQPIWFTLGILEALKGWDQGLKGMCVGEKRKLIIPPALGYGKEGKGIIPPEST
LIFNIDLLEIRNGPRSHESFQEMDLNDDWKLSKDEVKAYLKKEFEKHGAVVNESHHDALVED
IFDKEDDKDGFISAREFTYKHDEL

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 176-179

Casein kinase II phosphorylation site.

amino acids 143-146, 156-159, 178-181 and 200-203

Endoplasmic reticulum targeting sequence.

amino acids 208-211

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 78-114 and 118-131

EF-hand calcium-binding domain.

amino acids 191-203, 184-203 and 140-159

S-100/ICaBP type calcium binding domain

amino acids 183-203

FIGURE 54

AATAAAGCTTCCTTAATGTTGTATATGTCTTTGAAGTACATCCGTGCATTTTTTTTTTAGCAT
CCAACCATTCCTCCCTTGTAGTTCTCGCCCCCTCAAATCACCCCTCTCCCGTAGCCCAACCGA
CTAACATCTCAGTCTCTGAAAATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCT
CACGGGGCTCAGTCTCTTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTACAGTAC
CTGCCACCCCTCAACGTCCTCAATGGCTCTGACGCCCCGCTGCCCTGCACCTTCAACTCCTGC
TACACAGTGAACCACAAACAGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTC
TGAGGAGATGTTCTCCAGTTCCGCATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAG
ACCGCGTGGAGTTCTCAGGGAACCCAGCAAGTACGATGTGTGCGGTGATGCTGAGAAACGTG
CAGCCGGAGGATGAGGGGATTTACAACCTGCTACATCATGAACCCCCCTGACCGCCACCGTGG
CCATGGCAAGATCCATCTGCAGGTCCTCATGGAAGAGCCCCCTGAGCGGGACTCCACGGTGG
CCGTGATTGTGGGTGCCTCCGTGCGGGGCTTCTGGCTGTGGTCATCTTGGTGTGATGGTG
GTCAAGTGTGTGAGGAGAAAAAAGAGCAGAAGCTGAGCACAGATGACCTGAAGACCGAGGA
GGAGGGCAAGACGGACGGTGAAGGCAACCCGGATGATGGCGCCAAGTAGTGGGTGGCCGGCC
CTGCAGCCTCCCGTGTCCCGTCTCCTCCCCCTCTCCGCCCTGTACAGTGACCCTGCCTGCTCG
CTCTTGGTGTGCTTCCCGTGACCTAGGACCCCAAGGGCCACCTGGGGCCTCCTGAACCCCCG
ACTTCGTATCTCCCACCCTGCACCAAGAGTGACCCACTCTCTTCCATCCGAGAAACCTGCCA
TGCTCTGGGACGTGTGGGCCCTGGGGAGAGGAGAGAAAGGGCTCCACCTGCCAGTCCCTGG
GGGGAGGCAGGAGGCACATGTGAGGGTCCCCAGAGAGAAGGGAGTGGGTGGGCAGGGGTAGA
GGAGGGGCCGCTGTACCTGCCCAGTGCTTGCCTGGCAGTGGCTTCAGAGAGGACCTGGTGG
GGAGGGAGGGCTTTCCTGTGCTGACAGCGCTCCCTCAGGAGGGCCTTGGCCTGGCACGGCTG
TGCTCCTCCCCTGCTCCCAGCCCAGAGCAGCCATCAGGCTGGAGGTGACGATGAGTTCCTGA
AACTTGGAGGGGCATGTTAAAGGGATGACTGTGCATTCCAGGGCACTGACGGAAAGCCAGGG
CTGCAGGCAAAGCTGGACATGTGCCCTGGCCCAGGAGGCCATGTTGGGCCCTCGTTTCCATT
GCTAGTGGCCTCCTTGGGGCTCCTGTTGGCTCCTAATCCCTTAGGACTGTGGATGAGGCCAG
ACTGGAAGAGCAGCTCCAGGTAGGGGGCCATGTTTCCCAGCGGGGACCCACCAACAGAGGCC
AGTTTCAAAGTCAGCTGAGGGGCTGAGGGGTGGGGCTCCATGGTGAATGCAGGTTGCTGCAG
GCTCTGCCTTCTCCATGGGGTAACCAACCTCGCCTGGGCAGGGGCAGCCAAGGCTGGGAAAT
GAGGAGGCCATGCACAGGGTGGGGCAGCTTCTTTGGGGCTTCAGTGAGAACTCTCCCAGTT
GCCCTTGGTGGGGTTTTCCACCTGGCTTTTGGCTACAGAGAGGGAAGGGAAAGCCTGAGGCCG
GCATAAGGGGAGGCCTTGGAACCTGAGCTGCCAATGCCAGCCCTGTCCCATCTGCGGCCACG
CTACTCGCTCCTCTCCCAACAACCTCCCTTCGTGGGGACAAAAGTGACAATTGTAGGCCAGGC
ACAGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCGGGTGGATTACCTCCAT
CTGTTTAGTAGAAATGGGCAAAACCCCATCTCTACTAAAAATACAAGAATTAGCTGGGCGTG
GTGGCGTGTGCCTGTAATCCCAGCTATTTGGGAGGCTGAGGCAGGAGAATCGCTTGAGCCCG
GGAAGCAGAGGTTGCAGTGAACCTGAGATAGTGATAGTGCCACTGCAATTCAGCCTGGGTGAC
ATAGAGAGACTCCATCTCAAAAAAA

FIGURE 55

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45415

<subunit 1 of 1, 215 aa, 1 stop

<MW: 24326, pI: 6.32, NX(S/T): 4

MHRDAWLPRPAFSLTGLSLFFSLVPPGRSMEVTVPATLNVLNGSDARLPCTFNSCYTVNHKQ
FSLNWTYQECNNCSEEMFLQFRMKIINLKLERFQDRVEFSGNPSKYDVSVMRLRVQPEDEGI
YNCYIMNPPDRHRGHGKIHLQVLMEEPPERDSTVAVIVGASVGGFLAVVILVLMVVKCVRRK
KEQKLSTDDLKTEEEGKTDGEGNPDDGAK

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 161-179

Immunoglobulin-like fold:

amino acids 83-127

N-glycosylation sites.

amino acids 42-45, 66-69 and 74-77

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TOSTOT-2878/660

FIGURE 56

GTTGTATATGTCCTGAAGTACATCCGTGCATTTTTTTTAGCATCCAACCATCCTCCCTTGTA
GTTCTCGCCCCCTCAAATCACCTTCTCCCTTAGCCCCACCCNACTAACATCTCAGTCTCTGAA
AATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCTCACGGGGCTCAGTCTCTTTT
TCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCCACAGTACCTGNCCACCCTCAACGTCC
TCAATGGCTCTGACGCCCCGCTGCCCTGCCCTTCAACTCCTGCTACACAGTGAACCACAAAC
AGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTCTGAGGAGATGTTCTCCAG
TTCCGCATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAGACCGCGTGGAGTTCTCAGG
GAACCCCAGCAAGTACGATGTGTCGGTGATGCTGAGAAACGTGCAGCCGGAGGATGAGGGGA
TTTACAACCTGCTACATCATGAACCCCCC

09978187-101501
F05101-1818660

FIGURE 57

TCACGGGGCTCATCTCTTTTTCTCTTTGGTGCCCACCAGGACGGAGCATGGAGGTNCACATA
CCTGCCACCCTCAACGTCCTCAATGGCTTTGACGCCCCGCCTGCCCTGCACCTTCAACTCCNG
CTACACAGTGAACCACAAACAGTTCTCCCTGAACTGGATTTACCAGGAGTGCAACAACCTGGC
TCTGAGGAGATGTTCTCCAGTTCCCGCATGGAAGATCATTTAACCTGAAAGCTGGAAGCGG
TTTTCAAGAACCGCGTGGAAGTTTCTCAGGGAACCCCAGCAAGTACGATGTGTCTGGTGATGC
TGAGAAACGTGCAGCCGGAGGATGAGGGGATTTACAACTGCTACATCATGAACCCCCC

09978187-101501
T05T0T-28TB2650

FIGURE 58

TGC GGC GAC CGT CGT ACACCA **AT** GGG CCT CCACCTCCGCCCCCTACCGTGTGGGGCTGCTCCCGGATGGCCTCCTGT
 TCCTCTTGCTGCTGCTAATGCTGCTCGCGGACCCAGCGCTCCCGGCCGGACGTCAACCCCCAGTGGTGTGGTCC
 CTGGTGATTTGGGTAACCAACTGGAAGCCAAGCTGGACAAGCCGACAGTGGTGCATACCTCTGCTCCAAGAAGA
 CCGAAAGCTACTTACAAATCTGGCTGAACCTGGAACCTGCTGCTGCCTGTATCATTTGACTGCTGGATTGACAATA
 TCAGGCTGGTTTACAACAAAACATCCAGGGCCACCCAGTTTCTGATGGTGTGGATGTACGTGTCCCTGGCTTTG
 GGAAGACCTTCTCACTGGAGTTCTGGACCCAGCAAAAGCAGCGTGGGTTCCTATTTCCACACCATGGTGGAGA
 GCCTTGTGGGCTGGGGCTACACACGGGGTGAGGATGTCCGAGGGGCTCCCTATGACTGGCGCCGAGCCCCAAATG
 AAAACGGGCCCCCTACTTCTGGCCCTCCGCGAGATGATCGAGGAGATGTACCAGCTGTATGGGGGCCCCGTGGTGC
 TGGTTGCCCCACAGTATGGGCAACATGTACACGCTCTACTTTCTGCAGCGGCAGCCGAGGCCTGGAAGGACAAGT
 ATATCCGGGCCCTTCGTGTCACTGGGTGCGCCCTGGGGGGGCGTGGCCAAAGACCTGCGCGTCTTGGCTTCAGGAG
 ACAACAACCGGATCCAGTCATCGGGCCCCCTGAAGATCCGGGAGCAGCAGCGGTGAGCTGTCTCCACCAGCTGGC
 TGCTGCCCTACAACATACATGGTCACTGAGAAGGTGTTCTGTGCAGACACCCACAATCAACTACACACTGCGGG
 ACTACCGCAAGTTCTTCCAGGACATCGGCTTTGAAGATGGCTGGCTCATGCGGCAGGACACAGAAGGGCTGGTGG
 AAGCCACGATGCCACCTGGCGTGCAGCTGCACTGCCTCTATGGTACTGGCGTCCCCACACCAGACTCCTTCTACT
 ATGAGAGCTTCCCTGACCGTGACCCATAAAATCTGCTTTGGTGACGGCGATGGTACTGTGAACCTGAAGAGTGGCC
 TGCAGTGCCAGGCCTGGCAGAGCCGCCAGGAGCACCAGTGTGCTGTCAGGAGCTGCCAGGCAGCGAGCACATCG
 AGATGCTGGCCAACGCCACCACCTGGCCTATCTGAAACGTGTGCTCCTTGGGGCCCT**GA**CTCCTGTGCCACAGGA
 CTCCTGTGGCTCGGCCGTGGACCTGCTGTTGGCCTCTGGGGCTGTATGGCCCACGCGTTTTGCAAAGTTTGTGA
 CTCACCATTCAAGGCCCCGAGTCTTGGACTGTGAAGCATCTGCCATGGGGAAGTGTGTTTGTATCCTTTCTCT
 GTGGCAGTGAAGAAGGAAGAAATGAGAGTCTAGACTCAAGGGACACTGGATGGCAAGAATGCTGCTGATGGTGG
 ACTGCTGTGACCTTAGGACTGGCTCCACAGGGTGGACTGGCTGGGGCCCTGGTCCCAGTCCCTGCCTGGGGCCATG
 TGTCCCCCTATTCTGTGGGCTTTTCATACTTGCCTACTGGGCCCTGGCCCCGAGCCTTCTATGAGGGATGTT
 ACTGGGCTGTGGTCTGTATCCAGAGGTCCCAGGGATCGGCTCCTGGCCCCCTCGGGTGACCCCTTCCACACACCA
 GCCACAGATAGGCCTGCCACTGGTTCATGGGTAGCTAGAGCTGCTGGCTTCCCTGTGGCTTAGCTGGTGGCCAGCC
 TGAAGTGGCTTCTTGGGCGAGCCTAGTAGCTCCTGCAGGCAGGGGAGTTTGTGCGTTCTTCGTGGTCCCAGGC
 CCTGGGACATCTCACTCCACTCCTACCTCCCTTACCACCAGGAGCATTCAAGCTCTGGATTGGGCAGCAGATGTG
 CCCCCAGTCCCGCAGGCTGTGTTCCAGGGGCCCTGATTTCTCGGATGTGCTATTGGCCCCAGGACTGAAGCTGC
 CTCCCTTACCCTGGGACTGTGGTTCCAAGGATGAGAGCAGGGGTTGGAGCCATGGCCTTCTGGGAACCTATGGA
 GAAAGGGAATCCAAGGAAGCAGCCAAGGCTGCTCGCAGCTTCCCTGAGCTGCACCTCTTGCTAAACCCACCATCA
 CACTGCCACCCCTGCCCTAGGGTCTCACTAGTACCAAGTGGGTGAGCAGGGCTGAGGATGGGGCTCCTATCCAC
 CCTGGCCAGCACCCAGCTTAGTGCTGGGACTAGCCCAGAACTTGAATGGGACCCTGAGAGAGCCAGGGGTCCCC
 TGAGGCCCCCTAGGGGCTTTCTGTCTGCCCCAGGGTGCTCCATGGATCTCCCTGTGGCAGCAGGCATGGAGAGT
 CAGGGCTGCCTTCATGGCAGTAGGCTCTAAGTGGGTGACTGGCCACAGGCCGAGAAAAGGGTACAGCCTCTAGGT
 GGGGTTCCCAAAGACGCCCTTTCAGGCTGGACTGAGCTGCTCTCCACAGGGTTTCTGTGCAGCTGGATTTTCTCTG
 TTGCATACATGCCTGGCATCTGTCTCCCTTGTTCCTGAGTGGCCCCACATGGGGCTCTGAGCAGGCTGTATCTG
 GATTCTGGCAATAAAAGTACTCTGGATGCTGTAAAAA

097874501

FIGURE 59

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44189

><subunit 1 of 1, 412 aa, 1 stop

><MW: 46658, pI: 6.65, NX(S/T): 4

MGLHLRPYRVGLLPDGLLFLLLLLLMLLADPALPAGRHPVVLVPGDLGNQLEAKLDKPTVVH
YLCSKKTESYFTIWLNLLELLLPVIIDCWIDNIRLVYNKTSRATQFPDGVDVRVPGFGKTFSL
EFLDPSKSSVGSYFHTMVESLVGWGYTRGEDVRGAPYDWRRAPNENGPYFLALREMIEMYQ
LYGGPVVLVAHSMGNMYTLYFLQRQPQAWKDKYIRAFVSLGAPWGGVAKTLRVLASGDNNRI
PVIGPLKIREQQRSAVSTSWLLPYNITWSPEKVFVQTPPTINYTLRDYRKFFQDIGFEDGWLM
RQDTEGLVEATMPPGVQLHCLYGTGVPTPDSFYYESFPDRDPKICFGDGDGTVNLKSALQCQ
AWQSRQEHQVLLQELPGSEHIEMLANATTLAYLKRVLG

Important features:

Signal peptide:

amino acids 1-28

Potential lipid substrate binding site:

amino acids 147-164

N-glycosylation sites.

amino acids 99-102, 273-276, 289-292 and 398-401

Lipases, serine proteins

amino acids 189-201

Beta-transducin family Trp-Asp repeat

amino acids 353-365

09978187-101501

FIGURE 60

CGGACGCGTGGGCGGACGCGTGGGGCGGCGGCAGCGGCGGCGACGGCGACATGGGAGAGCGGG
GCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCA
GGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTG
AGGGCTACAGCAATGCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGAT
GCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGT
GGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTG
ACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTTGTTGGTTTTCTGCTTCCTACCAAC
CAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCAT
CACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCT
ACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACT
GCCTACGCCCTCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAA
CGCGGAGACCACCGAGGGCTACCAGCCGCCCCCTGTGTACTTGAGTGGCGGTTAGCGTGGGAA
GGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAAC TGCCA
GCCCCCTCTTTTACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCC
TGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCAGAGGGCTTCAGTCAGCCGCT
CACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCCTCGCTTTTAATGA
CCTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCCT
CAGCTTCCCCCGGCCCGGGTCAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAG
ACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCCTCA
CTCAGGTTTGCTTCCCCGTGTGCCCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGT
GGCCTCTGGGCTGCCTCCCGTGGTGTGAGGGCGGGGCTGGTGTCTCATGGCACTTCCTCCTTG
CTCCCACCCCTGGCAGCAGGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTC
TGCAGTTGTTACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGACTCTGTC
TGTGCCGAGTGTATTATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACG
GAATAAATGTTTTCTCATTCAAAG

FIGURE 61

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48304

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24810, pI: 4.75, NX(S/T): 1

MESGAYGAAGAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKQMYCVFN
RNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLIVIGDLLFSALWTFWLVGFC
FLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQNYVDPTP
DPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPVY

Important features:

Type II Transmembrane domain:

amino acids 1-45

Other transmembrane domains:

amino acids 74-90, 108-126 and 145-161

N-glycosylation site.

amino acids 97-100

09978187-101501
FOSTOT" 48787660

FIGURE 62

GAGCCACCTACCCTGCTCCGAGGCCAGGCCTGCAGGGCCTCATCGGCCAGAGGGTGATCAGTGAGCAGAAGGATG
 CCGGTGGCCGAGGCCCCCAGGTGGCTGGCGGGCAGGGGGACGGAGGTGATGGCGAGGAAGCGGAGCCAGAGGGG
 ATGTTCAAGGCCTGTGAGGACTCCAAGAGAAAAGCCCGGGGCTACCTCCGCCTGGTGCCCCCTGTTTGTGCTGCTG
 GCCCTGCTCGTGCTGGCTTCGGCGGGGGTGCTACTCTGGTATTTCTAGGGTACAAGGCGGAGGTGATGGTCAGC
 CAGGTGTACTCAGGCAGTCTGCGTGACTCAATCGCCACTTCTCCAGGATCTTACCCGCCGGGAATCTAGTGCC
 TTCCGCAGTGAAACCGCCAAAGCCCAGAAGATGCTCAAGGAGCTCATCACCAGCACCCGCCTGGGAACCTTACTAC
 AACTCCAGCTCCGTCTATTCTTGGGGAGGGACCCCTCACCTGCTTCTTCTGGTTTCATTCTCCAAATCCCCGAG
 CACCGCCGGCTGATGCTGAGCCCCGAGGTGGTGACGGCACTGCTGGTGGAGGAGCTGCTGTCCACAGTCAACAGC
 TCGGCTGCCGTCCCCTACAGGGCCGAGTACGAAGTGGACCCCGAGGGCCTAGTGATCCTGGAAGCCAGTGTGAAA
 GACATAGCTGCATTGAATTCCACGCTGGGTTGTTACCGCTACAGCTACGTGGGCCAGGGCCAGGTCTCCGGCTG
 AAGGGGCTGACCACCTGGCCTCCAGCTGCCTGTGGCACCTGCAGGGCCCCAAGGACCTCATGCTCAAACCTCCGG
 CTGGAGTGGACGCTGGCAGAGTGCCGGGACCGACTGGCCATGTATGACGTGGCCGGGCCCCCTGGAGAAGAGGCTC
 ATCACCCTCGGTGTACGGCTGCAGCCGCCAGGAGCCCGTGGTGGAGGTTCTGGCGTCCGGGGCCATCATGGCGGT
 GTCTGGAAGAAGGGCCTGCACAGCTACTACGACCCCTTCGTGCTCTCCGTGCAGCCGGTGGTCTTCCAGGCCTGT
 GAAGTGAACCTGACGCTGGACAACAGGCTCGACTCCAGGGCGTCTCAGACCCCGTACTTCCCCAGCTACTAC
 TCGCCCCAAACCCACTGCTCCTGGCACCTCACGGTGCCCTCTCTGGACTACGGCTTGGCCCTCTGGTTTGATGCC
 TATGCACTGAGGAGGCAGAAGTATGATTGCGGTGCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGT
 GGCTTGGCATCCTGCAGCCCTACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTACC
 TCCCAGATCTCCCTCACCGGGCCCCGTGTGCGGGTGCACTATGGCTTGTACAACAGTCCGACCCCTGCCCTGGA
 GAGTTCTCTGTTCTGTGAATGGACTCTGTGTCCCTGCCTGTGATGGGGTCAAGGACTGCCCCAACGGCCTGGAT
 GAGAGAACTGCGTTTGCAGAGCCACATTCAGTGCAAAGAGGACAGCACATGCATCTCACTGCCCAAGGTCTGT
 GATGGGCAGCCTGATTGTCTCAACGGCAGCGATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTACCC
 TTCCAGTGTGAGGACCGGAGCTGCGTGAAGAAGCCCAACCCGAGTGTGATGGGCGGCCCCGACTGCAGGGACGGC
 TCGGATGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCCCTCCAGCCGATTGTTGGTGGAGCTGTGTCTCCGAG
 GGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTCCGGGGTGCACACATCTGTGGGGGGGCCCTCATCGCTGACCGC
 TGGGTGATAACAGCTGCCCCTGCTTCCAGGAGGACAGCATGGCCTCCACGGTGTGTGGACCGTGTTCCTGGGC
 AAGGTGTGGCAGAAGTCCGCTGGCCTGGAGAGGTGTCCTTCAAGGTGAGCCGCTGCTCCTGCACCCGTACCAC
 GAAGAGGACAGCCATGACTACGACGTGGCGCTGCTGCAGCTCGACCACCCGGTGGTGGCTCGGCCGCCGTGCGC
 CCCGTCTGCCTGCCCGCGCGCTCCCACTTCTTCGAGCCCGGCTGCAGTGTGGATTACGGGCTGGGGCGCCTTG
 CGCGAGGGCGGCCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCAGTTGATCCACAGGACCTGTGCAGCGAG
 GCCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGCCGGCTACCGCAAGGGCAAGAAGGATGCCTGTGAGGGT
 GACTCAGGTGGTCCGCTGGTGTGCAAGGCACTCAGTGGCCGCTGGTTCTTGGCGGGGCTGGTCAGCTGGGGCCTG
 GGCTGTGGCCGGCCTAACTACTTCCGGCGTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGTG
 ACCTGAGGAAGTGGCCCCCTGCAAAGCAGGGCCACCTCCTGGACTCAGAGAGCCCAGGGCAACTGCCAAGCAGG
 GGGACAAGTATTCTGGCGGGGGGTGGGGGAGAGAGCAGGCCCTGTGGTGGCAGGAGGTGGCATCTTGTCTCGTCC
 CTGATGTCTGCTCCAGTGATGGCAGGAGGATGGAGAAGTGCCAGCAGCTGGGGGTCAAGACGTCCCCTGAGGACC
 CAGGCCCCACCCAGCCCTTCTGCCTCCCAATTCTCTCTCCTCCGTCCCCTTCTCCACTGCTGCCTAATGCAAG
 GCAGTGGCTCAGCAGCAAGAATGCTGGTTCTACATCCCGAGGAGTGTCTGAGGTGCGCCCCACTCTGTACAGAGG
 CTGTTTGGGCAGCCTTGCCTCCAGAGAGCAGATTCCAGCTTCGGAAGCCCCCTGGTCTAACTTGGGATCTGGGAAT
 GGAAGGTGCTCCCATCGGAGGGGACCTCAGAGCCCTGGAGACTGCCAGGTGGGCCTGCTGCCACTGTAAGCCAA
 AAGGTGGGGAAGTCTGACTCCAGGGTCTTGGCCCCACCCCTGCCTGCCACCTGGGCCCTCACAGCCCAGACCCT
 CACTGGGAGGTGAGCTCAGCTGCCCTTGGAAATAAGCTGCCTGATCAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 63

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49152

><subunit 1 of 1, 802 aa, 1 stop

><MW: 88846, pI: 6.41, NX(S/T): 7

MPVAEAPQVAGGQGDGGDGEAEPEGMFKACEDSKRKARGYLRLVPLFVLLALLVLASAGVL
LWYFLGYKAEVMVSQVYSGSLRVLNRHFSQDLTRRESSAFRSETAKAQKMLKELITSTRLGT
YYNSSSVYSFGEGPLTCFFWFILQIPEHRRMLLSPEVVQALLVEELLSTVNSSAAVPYRAEY
EVDPEGLVILEASVKDIAALNSTLGCYRYSYVGQGVLRRLKGPDLHLASSCLWHLQGPKDLML
KLRLEWTLAECDRLAMYDVAGPLEKRLITSVYGCSRQEPVVEVLASGAIMAVVWKKGLHSY
YDPFVLSVQPVVFQACEVNLTLDNRLDSQGVLSPTYFSPSYSPQTHCSWHLTVPSLDYGLAL
WFDAYALRRQKYDLPTQGGWTIQNRRLCGLRILQPYAERIPVVATAGITINFTSQISLTGP
GVRVHYGLYNQSDPCPGEFLLSVNGLCVPACDGVKDCPNGLDERNCVCRATFQCKEDSTCIS
LPKVCDGQPDCLNGSDEEQCQEGVPCGTFTFQCEDRSCVKKPNPQCDGRPDCRDGSDEEHCD
CGLQGPPSSRIVGGAVSSEGEWPWQASLQVRGRHICGGALIADRWVITAACFQEDSMASVT
WTVFLGKVVQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALQLDHPVVRSAAVRPVCLPA
RSHFFEPGLHCWITGWGALREGGPISNALQKVDVQLIPQDLCSEAYRYQVTPRMLCAGYRKG
KKDACQGDSSGGPLVCKALSGRWFLAGLVSWGLGCGRPNYFGVYTRITGVISWIQQVVT

Important features:

Type II transmembrane domain:

amino acids 46-67

Serine proteases, trypsin family, histidine active site.

amino acids 604-609

N-glycosylation sites.

amino acids 127-130, 175-178, 207-210, 329-332, 424-427, 444-447
and 509-512

Kringle domains.

amino acids 746-758 and 592-609

Homologous region to Kallikrein Light Chain:

amino acids 568-779

Homologous region to Low-density lipoprotein receptor:

amino acids 451-567

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FIGURE 64

GCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGTGGCTTGCGCATCCTGCAGCCC
TACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACCTCCCAGAT
CTCCCTCACCGGGCCCCGGTGTGCGGGTGC ACTATGGCTTGTACAACCAGTCGGACCCCTGCC
CTGGAGAGTTCTCTGTCTGTGAATGGACTCTGTGTCCCTGCCTGTGATGGGGTCAAGGAC
TGCCCCAACGGCCTGGATGAGAGAACTGCGTTTGAGAGCCACATTCCAGTGCAAAGAGGA
CAGCACATGCATCTCACTGCCCAAGGTCTGTGATGGGCAGCCTGATTGTCTCAACGGCAGCG
ATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTACCTTCCAGTGTGAGGACCGG
AGCTGCGTGAAGAAGCCCAACCCGCAGTGTGATGGGCGGCCCGACTGCAGGGACGGCTCGGA
TGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCCCTCCAGCCGCATTGTTGGTGGAGCTGTGT
CCTCCGAGGGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTGCGGGTTCGACACATCTGTGGG
GGGGCCCTCATCGCTGACCGCTGGGTGATAACAGCTGCCCCTGCTTCCAGGAGGACAGCAT
GGCCTCCACGGTGCTGTGGACCGTGTTCTTGGGCAAGGTGTGGCAGAACTCGCGCTGGCCTG
GAGAGGTGTCTTCAAGGTGAGCCGCCTGCTCCTGCACCCGTACCACGAAGAGGACAGCCAT
GACTACGACGTGGCGCTGCTGCAGCTCGACCACCCGGTGGTGCCTCGGCCGCCGTGCGCCC
CGTCTGCCTGCCCCGCGCTCCCACTTCTTCGAGCCCGGCTGCACTGCTGGATTACGGGCT
GGGGCGCCTTGCGCGAGGGCGGCCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCAGTTG
ATCCACAGGACCTGTGCAGCGAGGCCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGC
CGGCTACCGCAAGGGCAAGAAGGATGCCTGTGAGGTGACTCAGGTGGTCCGCTGGTGTGCA
AGGCACTCAGTGGCCGCTGGTTCTTGGCGGGGCTGGTCAGCTGGGGCCTGGGCTGTGGCCGG
CCTAACTACTTCGGCGTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGT
GACCTGAGGAACTGCCCCCTGCAAAGCAGGGCCACCTCCTGGACTCAGAGAGCCCAGGGC
AACTGCCAAGCAGGGGGACAAGTAT

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FIGURE 65

GGACGAGGGCAGATCTCGTTCTGGGGCAAGCCGTTGACACTCGCTCCCTGCCACCGCCCGGG
CTCCGTGCCGCCAAGTTTTTCATTTTCCACCTTCTCTGCCTCCAGTCCCCCAGCCCCTGGCCG
AGAGAAGGGTCTTACCGGCCGGGATTGCTGGAAACACCAAGAGGTGGTTTTTTGTTTTTAAA
ACTTCTGTTTTCTTGGGAGGGGGTGTGGCGGGGCAGGATGAGCAACTCCGTTCCCTCTGCTCTG
TTTCTGGAGCCTCTGCTATTGCTTTGCTGCGGGGAGCCCCGTACCTTTTGGTCCAGAGGGAC
GGCTGGAAGATAAGCTCCACAAACCCAAAGCTACACAGACTGAGGTCAAACCATCTGTGAGG
TTTAACCTCCGCACCTCCAAGGACCCAGAGCATGAAGGATGCTACCTCTCCGTGCGCCACAG
CCAGCCCTTAGAAGACTGCAGTTTCAACATGACAGCTAAAACCTTTTTTCATCATTACGGAT
GGACGATGAGCGGTATCTTTGAAAACCTGGCTGCACAACTCGTGTCAGCCCTGCACACAAGA
GAGAAAGACGCCAATGTAGTTGTGGTTGACTGGCTCCCCCTGGCCCACCAGCTTTACACGGA
TGCGGTCAATAATACCAGGGTGGTGGGACACAGCATTGCCAGGATGCTCGACTGGCTGCAGG
AGAAGGACGATTTTTCTCTCGGGAATGTCCACTTGATCGGCTACAGCCTCGGAGCGCACGTG
GCCGGGTATGCAGGCAACTTCGTGAAAGGAACGGTGGGCCGAATCACAGGTTTGGATCCTGC
CGGGCCCATGTTTGAAGGGGCCGACATCCACAAGAGGCTCTCTCCGGACGATGCAGATTTTG
TGGATGTCCTCCACACCTACACGCGTTCCTTCGGCTTGAGCATTGGTATTCAGATGCCTGTG
GGCCACATTGACATCTACCCCAATGGGGGTGACTTCCAGCCAGGCTGTGGACTCAACGATGT
CTTGGGATCAATTGCATATGGAACAATCACAGAGGTGGTAAAATGTGAGCATGAGCGAGCCG
TCCACCTCTTTGTTGACTCTCTGGTGAATCAGGACAAGCCGAGTTTTGCCTTCCAGTGCACT
GACTCCAATCGCTTCAAAAAGGGGATCTGTCTGAGCTGCCGCAAGAACCGTTGTAATAGCAT
TGGCTACAATGCCAAGAAAATGAGGAACAAGAGGAACAGCAAAATGTACCTAAAAACCCGGG
CAGGCATGCCTTTCAGAGGTAACCTTCAGTCCCTGGAGTGTCCCTTGAGGAAGGCCCTTAATA
CCTCCTTCTTAATACCATGCTGCAGAGCAGGGCACATCCTAGCCCAGGAGAAGTGGCCAGCA
CAATCCAATCAAATCGTTGCAAATCAGATTACACTGTGCATGTCCTAGGAAAGGGAATCTTT
ACAAAATAAACAGTGTGGACCCCTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAA

09078187-101501

FIGURE 66

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49646

><subunit 1 of 1, 354 aa, 1 stop

><MW: 39362, pI: 8.35, NX(S/T): 2

MSNSVPLLCFWSLCYCFAGSPVPFGPEGRLEDKLHKPKATQTEVKPSVRFNLRRTSKDPEHE
GCYLSVGHSQPLEDCSFNMTAKTFFIIHGWTMSGIFENWLHKLVSALHTREKDANVVVVDWL
PLAHQLYTDAVNNTRVVGHSIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGT
GRITGLDPAGPMFEGADIHKRLLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIYPNGGDF
QPGCGLNDVLGSIAYGTITEVVKCEHERAVHLFVDSLQNQDKPSFAFQCTDSNRFKKGICLS
CRKNRCNSIGYNAKKMRNKRNSKMYLKTTRAGMPFRGNLQSLECP

Important features:

Signal peptide:

amino acids 1-16

Lipases, serine active site.

amino acids 163-172

N-glycosylation sites.

amino acids 80-83 and 136-139

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FIGURE 67

CGGACGCGTGGGCGGACGCGTGGGCTGGGCAAGGGCCGGGGCGCCGGGCGGAGCCACCTCTTCCCCCTCCCCCGC
 TTCCCTGTGCGCTCCGCTGGCTGGACGCGCTGGAGGAGTGGAGCAGCACCCGGCCGGCCCTGGGGGCTGACAGT
 CGGCAAAGTTTGGCCCGAAGAGGAAGTGGTCTCAAACCCCGGCAGGTGGCGACCAAGGCCAGACCAGGGGCGCTCG
 CTGCCTGCGGGCGGGCTGTAGGCGAGGGCGCGCCCCAGTGCCGAGACCCGGGGCTTCAGGAGCCGGCCCCGGGAG
 AGAAGAGTGGCGGCGGCGGACGAGAGAAAACAACCTCAAAGTTGGCGAAAGGCACCGCCCCCTACTCCCGGGCTGCCG
 CCGCCTCCCCGCCCCCAGCCCTGGCATCCAGAGTACGGGTGAGCCCGGGCCATGGAGCCCCCTGGGGAGGCGG
 CACCAGGGAGCCTGGGCGCCCGGGGCTCCGCCGCGACCCCATCGGGTAGACCACAGAAGCTCCGGGACCCCTTCCG
 GCACCTCTGGACAGCCAGGATGCTGTTGGCCACCTCCTCCTCCTCCTCCTTGGAGGCGCTCTGGCCCATCCAG
 ACCGGATTATTTTCAAATCATGCTTGTGAGGACCCCCCAGCAGTGCTCTTAGAAGTGACAGGCACCTTACAGA
 GGCCCCCTGGTCCGGGACAGCCGCACCTCCCTGCCAACTGCACCTGGCTCATCCTGGGCAGCAAGGAACAGACTG
 TCACCATCAGGTTCCAGAAGCTACACCTGGCCTGTGGCTCAGAGCGCTTAACCCCTACGCTCCCTCTCCAGCCAC
 TGATCTCCCTGTGTGAGGCACCTCCCAGCCCTCTGCAGCTGCCCGGGGCAACGTACCATCACTTACAGCTATG
 CTGGGGCCAGAGCACCCATGGGCCAGGGCTTCTCTGCTCTCTACAGCCAAGATTGGCTGATGTGCCTGCAGGAAG
 AGTTTCAGTGCTGAACACCGCTGTGTATCTGCTGTCCAGCGCTGTGATGGGGTTGATGCCCTGTGGCGATGGCT
 CTCATGAAGCAGGTTGCAGCTCAGACCCCTTCCCTGGCCTGACCCCAAGACCCGTCCCTCCCTGCCCTTGCAATG
 TCACCTTGGAGGACTTCTATGGGGTCTTCTCCTCTCCTGGATATACACACCTAGCCTCAGTCTCCACCCCCCAGT
 CCTGCCATTGGCTGCTGGACCCCCATGATGGCCGGCGGCTGGCCGTGCGCTTACAGCCCTGGACTTGGGCTTTG
 GAGATGCAGTGCTGTATGACGGCCCTGGGCCCCCTGAGAGCTCCCGACTACTGCGTAGTCTCACCCACTTCA
 GCAATGGCAAGGCTGTCACTGTGGAGACACTGTCTGGCCAGGCTGTTGTGTCTACCACACAGTTGCTTGGAGCA
 ATGGTTCGTGGCTTCAATGCCACCTACCATGTGCGGGGCTATTGCTTGCCTTGGGACAGACCCCTGTGGCTTAGGCT
 CTGGCCTGGGAGCTGGCGAAGGCCTAGGTGAGCGCTGCTACAGTGAGGCACAGCGCTGTGACGGCTCATGGGACT
 GTGCTGACGGCACAGATGAGGAGGACTGCCCAGGCTGCCACCTGGACACTTCCCTGTGGGGCTGCTGGCACCT
 CTGGTGCCACAGCCTGCTACCTGCCTGCTGACCGCTGCAACTACCAGACTTTCTGTGCTGATGGAGCAGATGAGA
 GACGCTGTCCGCATTGCCAGCCTGGCAATTTCCGATGCCGGGACGAGAAGTGGTGTATGAGACGTGGGTGTGCG
 ATGGGCAGCCAGACTGTGCGGACGGCAGTGATGAGTGGGACTGCTCCTATGTTCTGCCCCGCAAGGTCATTACAG
 CTGCAGTCATTGGCAGCCTAGTGTGCGGCTGCTCCTGGTTCATCGCCCTGGGCTGCACCTGCAAGCTCTATGCCA
 TTCGACCCAGGAGTACAGCATCTTGGCCCCCTCTCCCGGATGGAGGCTGAGATTGTGCAGCAGCAGGCACCC
 CTTCTACGGGCAGCTCATTGCCCCAGGGTGCCATCCCACCTGTAGAAGACTTTCTACAGAGAATCCTAATGATA
 ACTCAGTGCTGGGCAACCTGCGTTCTCTGCTACAGATCTTACGCCAGGATATGACTCCAGGAGGTGGCCCAGGTG
 CCCGCCGTCGTGACGGGGCCGCTTGATGCGACGCCTGGTACGCCGTCTCCGCCGCTGGGCTTGTCTCCCTCGAA
 CCAACACCCCGGCTCGGGCCTCTGAGGCCAGATCCCAGGTACACCTTCTGCTGCTCCCCCTGAGGCCCTAGATG
 GTGGCACAGGTCCAGCCCGTGAGGGCGGGGCGAGTGGGTGGGCAAGATGGGGAGCAGGCACCCCCACTGCCCATCA
 AGGCTCCCTCCCATCTGCTAGCAGCTCTCCAGCCCCCACTACTGTCCCTGAAGCCCCAGGGCCACTGCCCTCAC
 TGCCCCCTAGAGCCATCACTATTGTCTGGAGTGGTGAGGCCCTGCGAGGCCGCTGTTGCCACGCTGGGGCCCC
 CAGGACCAACCCGAGCCCCCTGGACCCACACAGCAGTCTGGCCCTGGAAGATGAGGACGATGTGCTACTGG
 TGCCACTGGCTGAGCCGGGGGTGTGGGTAGCTGAGGCAGAGGATGAGCCACTGCTTACCTGAGGGGACCTGGGGG
 CTCTACTGAGGCCTCTCCCCCTGGGGGCTCTACTCATAGTGGCACAACCTTTTAGAGGTGGGTGAGCCTCCCTCC
 ACCACTTCCTTCCCTGTCCCTGGATTTTCAAGGACTTGGTGGGCCTCCCGTTGACCCTATGTAGCTGCTATAAAGT
 TAAGTGTCCCTCAGGCAGGGAGAGGGCTCACAGAGTCTCCTCTGTACGTGGCCATGGCCAGACACCCAGTCCCT
 TCACCACCACTGCTCCCCACGCCACCACTTTGGGTGGCTGTTTTTAAAAAGTAAAGTTCTTAGAGGATCATA
 GGTCTGGACACTCCATCCTTGCCAAACCTCTACCCAAAAGTGGCCTTAAGCACCGGAATGCCAATTAACCTAGAGA
 CCCTCCAGCCCCCAAGGGGAGGATTTGGGCAGAACCTGAGGTTTTGCCATCCACAATCCCTCTACAGGGCCTGG
 CTCACAAAAGAGTGCAACAAATGCTTCTATTCCATAGCTACGGCATTGCTCAGTAAGTTGAGGTCAAAAATAAA
 GGAATCATACATCTC

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FIGURE 68

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631

<subunit 1 of 1, 713 aa, 1 stop

<MW: 76193, pI: 5.42, NX(S/T): 4

MLLATLLLLLLGGALAHPDRIIFPNHACEDPPAVLLEVQGTQLQRPLVRDSRTSPANCTWLIL
GSKEQTVTIRFQKLHLACGSERLTLRSPLQPLISLCEAPPSPLQLPGGNVTITYSYAGARAP
MGQGFLLSYSQDWLMCLQEETFQCLNHRCVSAVQRCGDGVDACGDGSDEAGCSSDPFPGLTPRP
VPSLPCNVLTLEDYFYGVFSSPGYTHLASVSHQPQSCHWLLDPHDGRRRLAVRFTALDLGFGDAVH
VYDGPGPPESSRLLRSLTHFSNGKAVTVETLSGQAVVSYHTVAWSNGRGNATYHVRGYCLP
WDRPCGLGSGLGAGEGLGERCYSEAQRCDGSWDCADGTDEEDCPGCPPGHFPCGAAGTSGAT
ACYLPADRCNYQTFCADGADERRCRHCQPGNFRRCRDEKCVYETWVCDGQPD CADGSDEWDCS
YVLPKRVITA AVIGSLVCGLLLVIALGCTCKLYAIRTQEYSIFAPLSRMEAEIVQQQAPPSY
GQLIAQGAIPPVEDFP TENPNDNSVLGNLRSLLQILRQDMTPGGGPGARRRQGRMLMRRLVR
RLRRWGLLPRTNTPARASEARSQVTPSAAPLEALDGGTGPAREGGAVGGQDGEQAPPLPIKA
PLPSASTSPAPTTVPEAPGPLPSLPLEPSLLSGVVQALRGRLLP SLGPPGPTRSPPGPHTAV
LALEDEDDVLLVPLAE PGVWVAEAEDEPLLT

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 442-462

LDL-receptor class A (LDLRA) domain proteins

amino acids 411-431, 152-171, 331-350 and 374-393

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FIGURE 69

CGAGCTGGGCGAGAAGTAGGGGAGGGCGGTGCTCCGCCGCGGTGGCGGTTGCTATCGCTTCG
CAGAACCTACTCAGGCAGCCAGCTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCA
GACGCGATGGATAACGTGCAGCCGAAAATAAACATCGCCCCTTCTGCTTCAGTGTGAAAGG
CCACGTGAAGATGCTGCGGCTGGCACTAACTGTGACATCTATGACCTTTTTTATCATCGCAC
AAGCCCCTGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTTCATA
CTTTTATATGTACTCAGACTTGATCGATTAATGAAGTGGTTATTTTGGCCTTTGCTTGATAT
TATCAACTCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTTGGCACTGATACCAG
AAACCACAACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTCTT
GCCGACGGGGCCCTTATTTACCGGAAGCTTCTGTTCAATCCCAGCGGTCCTTACCAGAAAAA
GCCTGTGCATGAAAAAAAAGAAGTTTTGTAATTTTTATATTACTTTTTAGTTTGATACTAAGT
ATTAAACATATTTCTGTATTCTTCCAAAAAAAAAAAAAAAAAAAA

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FIGURE 70

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49645

><subunit 1 of 1, 152 aa, 1 stop

><MW: 17170, pI: 9.62, NX(S/T): 1

MDNVQPKIKHRPFCFSVKGHVKMLRLALTVTSM TFFIIAQAPEPYIVITGFEVTVILFFILL
YVLRDLRLMKWLFWPLLDIINSLVTTVFMLIVSVLALIPETTTLT VGGGVFALVTAVCCLAD
GALIYRKLLFNPSGPYQKKPVHEKKEVL

Important features:

Potential type II transmembrane domain:

amino acids 26-42

Other potential transmembrane domain:

amino acids 44-65, 81-101 and 109-129

Leucine zipper pattern

amino acids 78-99 and 85-106

N-myristoylation site.

amino acids 110-115

Ribonucleotide reductase large subunit protein

amino acids 116-127

FIGURE 71

GGGCGAGAAGTAGGGGAGGGCGTGTTCGCGCGCGGTGGCGGTTGCTATCGTTTTGCAGAACC
TACTCAGGCAGCCAGNTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCAGACGCGA
TGGATAACGTGCAGCCGAAAATAAAACATCGCCCCTTCTGCTTCAGTGTGAAAGGCCACGTG
AAGATGCTGCGGCTGGCACTAACTGNGACATCTATGACCTTTTTTATNATCGCACAAGCCCC
TGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTTTCATACTTTTAT
ATGTACTCAGACTTGATCGATTAATGAAGTGGTTATTTTGGCCTTTGCTTGATATTATCAAC
TCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTTGGCACTGATACCAGAAACCAC
AACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTNTTGCCGAC

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FIGURE 72

CAGCCCCGCGCGCCGGCCGAGTCGCTGAGCCGCGGCTGCCGGACGGGACGGGACCGGCTAGG
CTGGGCGCGCCCCCGGGCCCCGCGTGGGCATGGGCGCACTGGCCCCGGGCGCTGCTGCTGC
CTCTGCTGGCCCAGTGGCTCCTGCGCGCCGCCCGGAGCTGGCCCCCGCGCCCTTCACGCTG
CCCCTCCGGGTGGCCGCGGCCACGAACCGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCC
TGCCGAGCGCCACGCCGACGGCTTGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGG
GCGCCGCCAACTTCTTGCCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTAC
CTGGAGATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAG
TAACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGT
CTAGCACATACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACG
GGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTC
CATTGCCACTATTTTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATAC
TTGGCCTAGCTTATGCCCACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCC
CTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCC
CGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGT
ATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTG
AAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGC
CATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGG
AAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAG
CTGGCGTGCTGGACGAATTTCGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCT
GAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTACATTCAGC
CCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCCCATCCACAAAT
GCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAA
GAGGTGGGCTTCGCAGCGAGCCCCGTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTT
CCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAG
CCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTT
AATCGTCCTGCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCCCGTGACCCTGAGGTCGTCA
ATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAA
CCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGCAGCAGCCGGGATCGATGGTGGCG
CTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCTGCTCCAGATGCCTTCTAGATTAC
TGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATCCTCCCTACTTCCAAGAAAAATAATTAA
AAAAAAAACCTTCATTCTAA

FIGURE 73

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45493

><subunit 1 of 1, 518 aa, 1 stop

><MW: 56180, pI: 5.08, NX(S/T): 2

MGALARALLLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTPGPGTPAERHADGLAL
ALEPALASPAGAAANFLAMVDNLQGDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHS
YIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFESNF
FLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGS
LVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIVDSGTTLLR
LPQKVFDVAVEAVARASLIPEFSDGFWTGSQLACWTNSETPWSYFPKISIIYLRDENSRSFR
ITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCA
EIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCGAILLVLLVLLLLPFRC
QRRPRDPEVVNDESSLVRHRWK

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 466-494

N-glycosylation sites.

amino acids 170-173 and 366-369

Leucine zipper pattern.

amino acids 10-31 and 197-118

Eukaryotic and viral aspartyl proteases

amino acids 109-118, 252-261 and 298-310

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FIGURE 74

CGCCTCCGCCTTCGGAGGCTGACGCGCCCGGGCGCCGTTCCAGGCCTGTGCAGGGCGGATCG
GCAGCCGCCTGGCGGCGATCCAGGGCGGTGCGGGGCCTGGGCGGGAGCCGGGAGGCGCGGCC
GGCATGGAGGCGCTGCTGCTGGGCGCGGGGTTGCTGCTGGGCGCTTACGTGCTTGTCTACTA
CAACCTGGTGAAGGCCCCGCCGTGCGGCGGCATGGGCAACCTGCGGGGCCGCACGGCCGTGG
TCACGGGCGCCAACAGCGGCATCGGAAAGATGACGGCGCTGGAGCTGGCGCGCCGGGGAGCG
CGCGTGGTGCTGGCCTGCCGCAGCCAGGAGCGCGGGGAGGCGGCTGCCTTCGACCTCCGCCA
GGAGAGTGGGAACAATGAGGTCATCTTCATGGCCTTGGACTTGGCCAGTCTGGCCTCGGTGC
GGGCCTTTGCCACTGCCTTTCTGAGCTCTGAGCCACGGTTGGACATCCTCATCCACAATGCC
GGTATCAGTTCCTGTGGCCGGACCCGTGAGGCGTTTAACTGCTGCTTCGGGTGAACCATAT
CGGTCCCTTTCTGCTGACACATCTGCTGCTGCCTTGCTGAAGGCATGTGCCCTAGCCGCG
TGGTGGTGGTAGCCTCAGCTGCCCACCTGTCGGGGACGTCTTGACTTCAAACGCCTGGACCGC
CCAGTGGTGGGCTGGCGGCAGGAGCTGCGGGCATATGCTGACACTAAGCTGGCTAATGTACT
GTTTGGCCGGGAGCTCGCCAACCAGCTTGAGGCCACTGGCGTCACCTGCTATGCAGCCCACC
CAGGGCCTGTGAACTCGGAGCTGTTCTGCGCCATGTTCTGGATGGCTGCGCCCACTTTTG
CGCCCATTTGGCTTGGCTGGTGCTCCGGGCACCAAGAGGGGGTGCCAGACACCCCTGTATTG
TGCTCTACAAGAGGGCATCGAGCCCCCTCAGTGGGAGATATTTTGCCAACTGCCATGTGGAAG
AGGTGCCTCCAGCTGCCCAGACGACCGGGCAGCCCATCGGCTATGGGAGGCCAGCAAGAGG
CTGGCAGGGCTTGGGCCTGGGGAGGATGCTGAACCCGATGAAGACCCCCAGTCTGAGGACTC
AGAGGCCCCATCTTCTCTAAGCACCCCCCACCCTGAGGAGCCACAGTTTCTCAACCTTACC
CCAGCCCTCAGAGCTCACCAGATTTGTCTAAGATGACGCACCGAATTCAGGCTAAAGTTGAG
CCTGAGATCCAGCTCTCCTAACCCTCAGGCCAGGATGCTTGCCATGGCACTTCATGGTCCTT
GAAAACCTCGGATGTGTGTGAGGCCATGCCCTGGACACTGACGGGTTTGTGATCTTGACCTC
CGTGGTTACTTTCTGGGGCCCCAAGCTGTGCCCTGGACATCTCTTTTCTGGTTGAAGGAAT
AATGGGTGATTATTTCTTCTGAGAGTGACAGTAACCCAGATGGAGAGATAGGGGTATGCT
AGACACTGTGCTTCTCGGAAATTTGGATGTAGTATTTTCAGGCCCCACCCTTATTGATTCTG
ATCAGCTCTGGAGCAGAGGCAGGGAGTTTGCAATGTGATGCACTGCCAACATTGAGAATTAG
TGAAGTATCCCTTTGCAACCGTCTAGCTAGGTAGTTAAATTACCCCATGTTAATGAAGCG
GAATTAGGCTCCCGAGCTAAGGGACTCGCCTAGGGTCTCACAGTGAGTAGGAGGAGGGCCTG
GGATCTGAACCCAAGGGTCTGAGGCCAGGGCCGACTGCCGTAAGATGGGTGCTGAGAAGTGA
GTCAGGGCAGGGCAGCTGGTATCGAGGTGCCCCATGGGAGTAAGGGGACGCCTTCCGGGCGG
ATGCAGGGCTGGGGTCATCTGTATCTGAAGCCCCCTCGGAATAAAGCGCGTTGACCGCCAAA
AAAAAAAAAAAAAAAAAAAA

09978187-101504

FIGURE 75

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48227

<subunit 1 of 1, 377 aa, 1 stop

<MW: 40849, pI: 7.98, NX(S/T): 0

MEALLLGAGLLLGAYVLVYYNLVKAPPCGGMGNLRGRTAVVTGANSIGKMTALELARRGAR
VVLACRSQERGEAAAFDLRQESGNNEVIFMALDLASLASVRAFATAFLSSEPRLDILIHNAG
ISSCGRTREAFNLLLRVNHIGPFLLTHLLLPCLKACAPSRVVVVASAAHCRGRLDKRLDRP
VVGWRQELRAYADTKLANVLFARELANQLEATGVTCYAAHPGPVNSELFLRHVPGWLRPLLR
PLAWLVLRAPRGGAQTPLYCALQEGIEPLSGRYFANCHVEEVPPAARDDRAAHRLWEASKRL
AGLGPGEDAEPDEDPQSEDSEAPSSLSTPHPEEPTVSQPYPSPQSSPDLSKMTHRIQAKVEP
EIQLS

Important features:

Signal peptide:

amino acids 1-16

Glycosaminoglycan attachment site.

amino acids 46-49

Short-chain alcohol dehydrogenase family

amino acids 37-49 and 114-124

09978187-101501

FIGURE 76

GGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATCATGGGAGGCATGGCTCAG
GACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGACCAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGC
CAAGCCTCAGGCCAGCCACCTCCCACCATCCGCTGGTTGCTGAATGGGCAGCCCCCTGAGCATGGTGGCCCCAGAC
CCACACCACCTCCTGCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCACAGATGGCCAG
GCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGCAGTCAGCAGAGGCGCT
CGGCTGTCTGTGGCTGTCTCCGGGAGGATTTCCAGATCCAGCCTCGGGACATGGTGGCTGTGGTGGGTGAGCAG
TTTACTCTGGAATGTGGGCCGCCCTGGGGCCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTG
GCCCTCCAGCCCCGAAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGGG
ACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCCGCGCAGCCCCGGGTTTCCATCCAGGAGCCC
CAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTCAGCTGGAAAATGTGACACTGCTGAACCCGGAT
CCTGCAGAGGGCCCCAAGCCTAGACCGGCGGTGTGGCTCAGCTGGAAGGTGAGTGGCCCTGCTGCGCCTGCCCAA
TCTTACACGGCCTTGTTCAGGACCCAGACTGCCCCGGGAGGCCAGGGAGCTCCGTGGGCAGAGGAGCTGCTGGCC
GGCTGGCAGAGCGCAGAGCTTGGAGGCCTCCACTGGGGCCAAGACTACGAGTTCAAAGTGAGACCATCCTCTGGC
CGGGCTCGAGGCCCTGACAGCAACGTGCTGCTCCTGAGGCTGCCGGAAGAGTGGCCAGTGCCCCACCTCAGGAA
GTGACTCTAAAGCCTGGCAATGGCACTGTCTTTGTGAGCTGGGTCCCACCACCTGCTGAAAACCAATGGCATC
ATCCGTGGCTACCAGGTCTGGAGCCTGGGCAACACATCACTGCCACCAGCCAACCTGGACTGTAGTTGGTGAGCAG
ACCCAGCTGGAATCGCCACCCATATGCCAGGCTCCTACTGCGTGCAAGTGGCTGCAGTCACTGGTGTGGAGCT
GGGGAGCCAGTAGACCTGTCTGCCTCCTTTTAGAGCAGGCCATGGAGCGAGCCACCCAAGAACCAGTGAGCAT
GGTCCCTGGACCCTGGAGCAGCTGAGGGCTACCTTGAAGCGGCCTGAGGTGATGCCACCTGCGGTGTTGCACTC
TGGCTGCTGCTTCTGGGCACCGCCGTGTGTATCCACCGCCGGCGCGAGCTAGGGTGACCTGGGCCCAGGTCTG
TACAGATATACAGTGAGGATGCCATCCTAAAACACAGGATGGATCACAGTGACTCCAGTGGTTGGCAGACACT
TGGCGTTCCACCTCTGGCTCTCGGGACCTGAGCAGCAGCAGCAGCCTCAGCAGTGGCTGGGGGGCGGATGCCCGG
GACCCACTAGACTGTGCTCGCTCCTTGCTCTCCTGGGACTCCCGAAGCCCCGGCGTGCCCCCTGCTTCCAGACACC
AGCACTTTTATGGCTCCCTCATCGCTGAGCTGCCCTCCAGTACCCAGCCAGGCCAAGTCCCCAGGTCCCAGCT
GTCAGGCGCCTCCCACCCAGCTGGCCAGCTCTCCAGCCCCTGTTCCAGCTCAGACAGCCTCTGCAGCCGCAGG
GGACTCTCTTCTCCCCGCTTGTCTCTGGCCCCTGACAGAGGCTTGAAGGCCAAAAGAGCAGGAGCTGCAGCAT
GCCAACAGTTCCCCACTGCTCCGGGGCAGCCACTCCTTGGAGCTCCGGGCCCTGTGAGTTAGGAAATAGAGGTTCC
AAGAACCTTTCCCAAAGCCCAGGAGCTGTGCCCAAGCTCTGGTTGCCTGGCGGGCCCTGGGACCGAAACTCTC
AGCTCCTCAAATGAGCTGGTTACTCGTCATCTCCTCCAGCACCCCTCTTTCTCATGAAACTCCCCCAACTCAG
AGTCAACAGACCCAGCCTCCGGTGGCACCACAGGCTCCCTCCTCCATCCTGCTGCCAGCAGCCCCCATCCCCATC
CTTAGCCCCCTGCAGTCCCCCTAGCCCCCAGGCCTCTTCCCTCTCTGGCCCCAGCCCAGCTTCCAGTCGCTGTCC
AGCTCCTCACTGTATCCTTGGGGGAGGATCAAGACAGCGTGTGACCCCTGAGGAGGTAGCCCTGTGCTTGGAA
CTCAGTGAGGGTGAGGAGACTCCAGGAACAGCGTCTCTCCATGCCAAGGGCTCCTTACCCCCCACCACCTAT
GGGTACATCAGCGTCCCAACAGCCTCAGAGTTACCGGACATGGGCAGGACTGGAGGAGGGGTGGGGCCCAAGGGG
GGAGTCTTGCTGTGCCACCTCGGCCCTGCCTCACCCCCACCCCCAGCGAGGGCTCCTTAGCCAATGGTTGGGGC
TCAGCCTCTGAGGACAATGCCGCCAGCGCCAGAGCCAGCCTTGTGAGCTCCTCCGATGGCTCCTTCTCGCTGAT
GCTCACTTTGGCCGGGCCCTGGCAGTGGCTGTGGATAGCTTTGGTTTCGGTCTAGAGCCCAGGGAGGCAGACTGC
GTCTTCATAGATGCCTCATCACCTCCCTCCCCACGGGATGAGATCTTCTGACCCCCAACCTCTCCCTGCCCTG
TGGGAGTGAGGCCAGACTGGTTGGAAGACATGGAGGTGAGCCACACCAGCGGCTGGGAAGGGGGATGCCCTCCC
TGGCCCCCTGACTCTCAGATCTCTTCCAGAGAAGTCAGCTCCACTGTGCTATGCCCAAGGCTGGTGTCTCTCCT
GTAGATTACTCTGAACCGTGTCCCTGAGACTTCCAGACGGGAATCAGAACCCTTCTCCTGTCCACCACAAG
ACCTGGGCTGTGGTGTGTGGGTCTTGGCCTGTGTTTCTCTGCAGCTGGGGTCCACCTTCCCAAGCCTCCAGAGAG
TTCTCCCTCCACGATTGTGAAAACAAATGAAAACAAATTAGAGCAAAGCTGACCTGGAGCCCCCAGGGAGCAAA
ACATCATCTCCACCTGACTCCTAGCCACTGCTTTCTCCTCTGTGCCATCCACTCCACCACCAGGTTGTTTGGC
CTGAGGAGCAGCCCTGCCTGCTGCTCTTCCCCCACCATTGGATCACAGGAAGTGAGGAGCCAGAGGTGCCCTT
GTGGAGGACAGCAGTGGCTGCTGGGAGAGGGCTGTGGAGGAAGGAGCTTCTCGGAGCCCCCTCTCAGCCTTACCT
GGGCCCCCTCCTCTAGAGAAGAGCTCAACTCTCTCCCAACCTCACCATGGAAAGAAAATAATTATGAATGCCACTG
AGGCACTGAGGCCCTACCTCATGCCAAACAAAGGGTTCAAGGCTGGGTCTAGCGAGGATGCTGAAGGAAGGGAGG
TATGAGACCGTAGGTCAAAGCACCATCCTCGTACTGTTGTCACTATGAGCTTAAGAAATTTGATACCATAAAT
GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 77

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41404

<subunit 1 of 1, 985 aa, 1 stop

<MW: 105336, pI: 6.55, NX(S/T): 7

MGGMAQDSPPQILVHPQDQLFQGPGRMSCQASGQPPPTIRWLLNGQPLSMVPPDPHHLLP
DGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDM
VAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQGRHTVSGGSLLMARAEKSDEGTYMCV
ATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLNPDPAEGPKPRPAVWLSWKV
SGPAAPAQSYTALFRTQTAPGGQGAPWAEELLAGWQSAELGGLHWGQDYEFKVRPSSGRARG
PDSNVLLRLPEKVPSAPPQEVTLKPGNGTVFVSWVPPPAENHNGIIRGYQVWSLGNLTLPP
ANWTVVGEQTQLEIATHMPGSYCVQVAAVTGAGAGEPSRPVCLLLEQAMERATQEPSEHGPW
TLEQLRATLKRPEVIATCGVALWLLLLGTAVCIHRRRRARVHLGPGLYRYTSEDAILKHRMD
HSDSQWLADTWRSTSGSRDLSSSSSLSSRLGADARDPLDCRRSLLSWDSRSPGVPLLPDTST
FYGLIAELPSSTPARPSPQVPAVRRLPPQLAQLSSPCSSSDSLCSRRGLSSPRLSLAPAEA
WKAKKKQELQHANSPLLRGSHSLELRACELGNRGSKNLSQSPGAVPQALVAWRALGPKLLS
SSNELVTRHLPPAPLFPHETPPTQSQQQTQPPVAPQAPSSILLPAAPIPILSPCSPSPQASS
LSGPSPASSRLSSSSSLSSLGEDQDSVLTPEEVALCLELSEGEETPRNSVSPMPRAPSPPTTY
GYISVPTASEFTDMGRTGGGVGPKGGVLLCPRPCLTPTPSEGLANGWGSASEDNAASARA
SLVSSSDGSFLADAHFARALAVAVDSFGFGLPREADCVFIDASSPPSPRDEIFLTPNLSLP
LWEWRPDWLEDMEVSHTQRLGRGMPPWPPDSQISSQRSQLHCRMPKAGASPDYS

Important features:

Transmembrane domain:

amino acids 448-467

N-glycosylation sites:

amino acids 224-227, 338-341, 367-370, 374-377, 658-661 and 926-929

N-myristoylation sites.

amino acids 47-52, 80-85, 88-93, 99-104, 105-110, 181-186, 272-277, 290-295, 355-360, 403-408, 462-467, 561-566, 652-657, 849-854 and 876-881

Phosphotyrosine interaction domain proteins

amino acids 740-753

FIGURE 78

CTCCACGGTGTCCAGCGCCCAGAAATGCGGCTTCTGGTCTGCTATGGGGTTGCCTGCTGCT
CCCAGGTTATGAAGCCCTGGAGGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT
CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT
GGGATCCTCTTCTCTCGCTGCTCTGGCACCATCTATGCAGAAGAAGAAGGCCAGGAGACAAT
GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCCTGTGGA
ACCTCACCCCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG
TCTTTACTGATCTCTCTGTTTCGTCTTTCCAGGACCCTGCTGTCTCCTCCCCTTCTCCCAC
CTTCCAGCCTCTGGCTACAACACGCCTGCAGCCCAAGGCAAAAGCTCAGCAAACCCAGCCCC
CAGGATTGACTTCTCCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG
GCTGAGGCCCCCTCATTGCCAGGGACTTCCCAGTACGGGCACGAAAGGACTTCTCAGTACAC
AGGAACCTCTCCTCACCCAGCGACCTCTCCTCCTGCAGGGAGCTCCCGCCCCCCCCATGCAGC
TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGG
GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCTTGGTGTGCTGAGCCTTCTGTGAGC
CGCAGGCCTGATCGCCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCA
CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCACGCTTGACTGCGGAGGAAAAGGAAGCC
CCTTCCCAGGCCCCCTGAGGGGGACGTGATCTCGATGCCTCCCCTCCACACATCTGAGGAGGA
GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCCTGGCCAGGCCAGCAGT
GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTTCACCTCAGCCTCAGAG
TCCAGCTGCCCCGACTCCAGGGCTCTCCCCACCCTCCCAGGCTCTCCTCTTGATGTTCCA
GCCTGACCTAGAAGCGTTTGTGAGCCCTGGAGCCCAGAGCGGTGGCCTTGCTCTTCCGGCTG
GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCTCA
GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCCTGGGC
CTCATGCCCAGTGTGCGACCCTGCCTTCCCTCCACTCCAGACCCCACCTTGTCTTCCCTCCC
TGGCGTCTCAGACTTAGTCCCACGGTCTCCTGCATCAGCTGGTGTGATGAAGAGGAGCATGCT
GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACCTGCATCCAGCCCTTCAGGAAGCCT
GTGAAAAACGTGATTCTTGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG
GACTCTGAATTCTAACAATGCCAGTGAAGTGTGCACTTGAGTTTGAGGGCCAGTGGGCCTG
ATGAACGCTCACACCCCTTCAGCTTAGAGTCTGCATTTGGGCTGTGACGTCTCCACCTGCCC
CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGACTCCCCTGAGGCCTGCTAAG
TCCAGGCCTTGGTCAGGTGAGGTGCACATTGCAGGATAAGCCCAGGACCGGCACAGAAGTGG
TTGCCTTTNCCATTTGCCCTCCCTGGNCCATGCCTTCTTGCCTTTGGAAAAAATGATGAAGA
AAACCTTGGCTCCTTCCCTTGTCTGGAAAGGGTACTTGCCTATGGGTTCTGGTGGCTAGAGA
GAAAAGTAGAAAACAGAGTGCACGTAGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCGG
ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTGCGGGGTGGTGGTAAAGTA
GCACAACTACTATTTTTTTTTCTTTTTCCATTATTATTGTTTTTTAAGACAGAATCTCGTGCT
GCTGCCCAGGCTGGAGTGCAGTGGCACGATCTGCAAACCTCCGCCTCCTGGGTTCAAGTGATT
CTTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCACCACCACACCTGGCTAATT
TTTGTACTTTTAGTAGAGATGGGGTTTACCATTGTTGGCCAGGCTGGTCTTGAACCTCTGAC
CTCAAATGAGCCTCCTGCTTCAGTCTCCCAAATTGCCGGGATTACAGGCATGAGCCACTGTG
TCTGGCCCTATTTCTTTTAAAAAGTGAAATTAAGAGTTGTTTCAATATGCAAACTTGGAAG
ATGGAGGAGAAAAAGAAAAGGAAGAAAAAATGTCACCCATAGTCTCACCAGAGACTATCAT
TATTTTCGTTTTGTTGTAATTTCTTCCACTCTTTTCTTCTTACATAATTTGCCGGTGTCTT
TTTACAGAGCAATTATCTTGTATATACAATTTGTATCCTGCCTTTTCCACCTTATCGTTCC
ATCACTTTATTCCAGCACTTCTCTGTGTTTTACAGACCTTTTATAAATAAAATGTTTCATCA
GCTGCATAAAAAAAAAAAAAA

FIGURE 79

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS
GTIYAEEEGQETMKGRVSIIRDSRQELSLIVTLWNLTQLDAGEYWCGVEKRGPDDESLLISLFV
FPGPCCPPSPSPPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPG
TSQYGHERTSQYTGTSPHPATSPAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSI PMVRI
LAPVLVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWLSRLTAEKEAPSQAPEGD
VISMPPLHTSEEEELGFSKFVSA

Important features:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128

09978187 101504

FIGURE 80

TTGTGACTAAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGGTGGCAGGA
GCCGCAGAGCCAGAGCAGACAGCCGAGAAACAGGTGGACAGTGTGAAAGAACCAGTGGTCTC
GCTCTGTTGCCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCT
GGACTTGAGAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACTCAA
GCCCTGTTTCTTCTCCTTCTGTGAGTGGACCACGGAGGCTGGTGAGCTGCCTGTCTATCCCAA
AGCTCAGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCCGCCGGCATAGAAGCCAGGAG
CAGGGCTCTCAGAAGGCGGTGGTGCCAGCTGGGATCATGTTGTTGGCCCTGGTCTGTCTGC
TCAGCTGCCTGCTACCCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAACTGGCCAGAGTG
CTACATGACTTCGGGCTGGACGGATACCGGGGATACAGCCTGGCTGACTGGGTCTGCCTTGC
TTATTTCAACAAGCGGTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACA
ACGGGATCTTCCAGATCAACAGCCGGAGGTGGTGAGCAACCTCACCCCGAACGTCCCCAAC
GTGTGCCGGATGTACTGCTCAGATTTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGC
CATGAAGATAACCCAAGAGCCTCAGGGTCTGGGTACTGGGAGGCCTGGAGGCATCACTGCC
AGGGAAAAGACCTCACTGAATGGGTGGATGGCTGTGACTTCTTAGGATGGACGGAACCATGCA
CAGCAGGCTGGGAAATGTGGTTTGGTTCCTGACCTAGGCTTGGAAGACAAGCCAGCGAATA
AAGGATGGTTGAACGTGAAA

09978187-101501
T095T07-28782660

FIGURE 81

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52187

<subunit 1 of 1, 146 aa, 1 stop

<MW: 16430, pI: 5.05, NX(S/T): 1

MLLALVCLLSCLLPSSSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALD
YEADGSTNNGIFQINSRRWCSNLTNPVNPVCRMVCSDLLNPNLKDTVICAMKITQEPQGLGY
WEAWRHHCQGKDLTEWVDGCD

Important features:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 67-72

Homologous region to Alpha-lactalbumin / lysozyme C proteins.

amino acids 34-58 (catalytic domain), 111-132 and 66-107

09978187.101501

FIGURE 82

AGCCGCTGCCCCGGGCGGGCGCCCGCGGCGGCACCATGAGTCCCCGCTCGTGCCTGCGTTC
GCTGCGCCTCCTCGTCTTCGCCGTCTTCTCAGCCGCCGCGAGCAACTGGCTGTACCTGGCCA
AGCTGTCGTCCGTGGGGAGCATCTCAGAGGAGGAGACGTGCGAGAACTCAAGGGCCTGATC
CAGAGGCAGGTGCAGATGTGCAAGCGGAACCTGGAAGTCATGGACTCGGTGCGCCGCGGTGC
CCAGCTGGCCATTGAGGAGTGCCAGTACCAGTTCCGGAACCGGCGCTGGAAGTGTCCACAC
TCGACTCCTTGCCCGTCTTCGGCAAGGTGGTGACGCAAGGGACTCGGGAGGCGGCCTTCGTG
TACGCCATCTCTTCGGCAGGTGTGGCCTTTGCAGTGACGCGGGCGTGACAGTGGGGAGCT
GGAGAAGTGCGGCTGTGACAGGACAGTGATGGGGTCAGCCACAGGGCTTCCAGTGGTCAG
GATGCTCTGACAACATCGCCTACGGTGTGGCCTTCTCACAGTCGTTTGTGGATGTGCGGGAG
AGAAGCAAGGGGGCCTCGTCCAGCAGAGCCCTCATGAACCTCCACAACAATGAGGCCGGCAG
GAAGGCCATCCTGACACACATGCGGGTGGAATGCAAGTGCCACGGGGTGTCAGGCTCCTGTG
AGGTAAAGACGTGCTGGCGAGCCGTGCCGCCCTTCCGCCAGGTGGGTACGCACTGAAGGAG
AAGTTTGATGGTGCCACTGAGGTGGAGCCACGCCGCGTGGGCTCCTCCAGGGCACTGGTACC
ACGCAACGCACAGTTCAAGCCGCACACAGATGAGGACCTGGTGTACTTGGAGCCTAGCCCCG
ACTTCTGTGAGCAGGACATGCGCAGCGGCGTGCTGGGCACGAGGGGGCCGCACATGCAACAAG
ACGTCCAAGGCCATCGACGGCTGTGAGCTGCTGTGCTGTGGCCGCGGCTTCCACACGGCGCA
GGTGGAGCTGGCTGAACGCTGCAGCTGCAAATTCCACTGGTGCTGCTTCGTCAAGTGCCGGC
AGTGCCAGCGGCTCGTGGAGTTGCACACGTGCCGATGACCGCCTGCCTAGCCCTGCGCCGGC
AACCACCTAGTGGCCCAGGGAAGGCCGATAATTTAAACAGTCTCCACCACCTACCCCAAGA
GATACTGGTTGTATTTTTTTGTTCTGGTTTGGTTTTTGGGTCCTCATGTTATTTATTGCCGAA
ACCAGGCAGGCAACCCCAAGGGCACCAACCAGGGCCTCCCCAAAGCCTGGGCCTTTGTGGCT
GCCACTGACCAAAGGGACCTTGCTCGTGCCGCTGGCTGCCCCGATGTGGCTGCCACTGACCA
CTCAGTTGTTATCTGTGTCCGTTTTTCTACTTGACAGACCTAAGGTGGAGTAACAAGGAGTAT
TACCACCACATGGCTACTGACCGTGTATCGGGGAAGAGGGGGCCTTATGGCAGGGAAAATA
GGTACCGACTTGATGGAAGTCACACCCTCTGGAAAAAAGAACTCTTAACCTCTCCAGCACACA
TACACATGGACTCCTGGCAGCTTGAGCCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAGG
GAACAAGCAGATACCAGGTCAAGGGCACAGGTTTCAATTCAGCCCTTACATGGACAGCTAGA
GGTTCGATATCTGTGGGTCCTTCCAGGCAAGAAGAGGGAGATGAGAGCAAGAGACGACTGAA
GTCCACCCCTAGAACCCAGCCTGCCCCAGCCTGCCCCCTGGGAAGAGGAACTTAACCACTCC
CCAGACCCACCTAGGCAGGCATATAGGCTGCCATCCTGGACCAGGGATCCCGGCTGTGCCTT
TGCAGTCATGCCCCGAGTCACCTTTCACAGCGCTGTTCTCCTCATGAACTGAAAAACACACAC
ACCTGCGAGA
GAGAGGGAGGAAAGGGCTGTGCCCTTTCAGTCATGCCCCAGTCACCTTTCACAGCACTGTTCTC

FIGURE 83

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48328

<subunit 1 of 1, 351 aa, 1 stop

<MW: 39052, pI: 8.97, NX(S/T): 2

MSPRSCLRSLRLLVFAVFSAAASNWLYLAKLSSVGSISEEETCEKLGKGLIQRVQMCKRNLE
VMDSVRRGAQLAIEECQYQFRNRRWNCSTLDSLVPVFGKVVTQGTREAAFVYAISSAGVAFV
TRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYGVAFSQSFVDVRERSKGASSSRALM
NLHNNEAGRKAILTMRVECKCHGVSGSCEVKTCWRAVPPFRQVGHALKEKFDGATEVEPRR
VGSSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGRTCNKTSKAIDGCELLC
CGRGFHTAQVELAERCSCKFHWCCFVKCRQCQRLVELHTCR

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation sites.

amino acids 88-91 and 297-300

Wnt-1 family signature.

amino acids 206-215

Homologous region to Wnt-1 family proteins

amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

10978137.101501

FIGURE 84

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCAT
CGCCATGGACACCACCAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGGTCCCCGGAGGGC
CCTGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGTCCTGGTC
ACCACAGTCCTTTGGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCCTCCACGGAGCGCGC
GGCGCTGCTTGACGGCCACGACCTGCTGAGGACAAACGCCTCGAAGCAGACGGCGGGCGCTGG
GTGCCCTGAAGGAGGAGGTCCGAGACTGCCACAGCTGCTGCTCGGGGACGCAGGCGCAGCTG
CAGACCACGCGCGCGGAGCTTGGGGAGGCGCAGGCGAAGCTGATGGAGCAGGAGAGCGCCCT
GCGGGAAGTGCCTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGGCAGGGGCCGTGAGGACG
TCCGCACTGAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACAACTCCTGCGAGCCG
TGCCCCACGTCGTGGCTGTCCTTCGAGGGCTCCTGCTACTTTTTCTCTGTGCCAAAGACGAC
GTGGGCGGCGGCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTGATCGTTGGGGGCC
TGGATGAGCAGGGCTTCCTCACTCGGAACACGCGTGGCCGTGGTTACTGGCTGGGCCTGAGG
GCTGTGCGCCATCTGGGCAAGGTTTCAGGGCTACCAGTGGGTGGACGGAGTCTCTCTCAGCTT
CAGCCACTGGAACCAGGGAGAGCCCAATGACGCTTGGGGGCGCGAGAACTGTGTGTCATGATGC
TGCACACGGGGCTGTGGAACGACGCACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAG
AAAAGGCACAACTGCTTGACCCCGCCCAGTGCCCTGGAGCCGCGCCCATTGCAGCATGTCGTA
TCCTGGGGGCTGCTCACCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTTCTTCCT
CATCCACCGCTGCTGAGTCTCAGAAACACTTGGCCCAACATAGCCCTGTCCAGCCCAGTGCC
TGGGCTCTGGGACCTCCATGCCGACCTCATCCTAACTCCACTCACGCAGACCCAACCTAACC
TCCACTAGCTCCAAAATCCCTGCTCCTGCGTCCCCGTGATATGCCTCCACTTCTCTCCCTAA
CCAAGGTTAGGTGACTGAGGACTGGAGCTGTTTGGTTTTCTCGCATTTTCCACCAAACCTGGA
AGCTGTTTTTGCAGCCTGAGGAAGCATCAATAAATATTTGAGAAATGAAAAA

09978187-10501

FIGURE 85

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56352

<subunit 1 of 1, 293 aa, 1 stop

<MW: 32562, pI: 6.53, NX(S/T): 2

MDTTRYSKWGGSSSEVPGGPWGRVHWSRRPLFLALAVLVTTVLWAVILSILLSKASTERAA
LLDGHDLLRTNASKQTAALGALKEEVGDCHSCSGTQAQLQTTRAELGEAQAKLMEQESALR
ELRERV TQGLAEAGRGREDVRTELFRAL EAVRLQNN SCEPCPTSWLSFEGSCYFFSVPKTTW
AAAQDHCADASAH LVIVGGLDEQGF LTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVSL SFS
HWNQGE PNDAWGREN CVMMLHTGLWNDAPCDSEKDGWICEKRHNC

Important features:

Type II transmembrane domain:

amino acids 31-54

N-glycosylation sites.

amino acids 73-76 and 159-162

Leucine zipper pattern.

amino acids 102-123

N-myristoylation sites.

amino acids 18-23, 133-138 and 242-247

C-type lectin domain signature.

amino acids 264-287

09978187-10501
"FOR" 287650

FIGURE 86

GCCAGGGGAAGAGGGTGATCCGACCCGGGGAAGGTCGCTGGGCAGGGCGAGTTGGGAAGCG
GCAGCCCCCGCCGCCCCCGCAGCCCCTTCTCCTCCTTTCTCCACGTCCTATCTGCCTCTCG
CTGGAGGCCAGGCCGTGCAGCATCGAAGACAGGAGGAACTGGAGCCTCATTGGCCGGCCCCGG
GGCGCCGGCCTCGGGCTTAAATAGGAGCTCCGGGCTCTGGCTGGGACCCGACCGCTGCCGGC
CGCGCTCCCGCTGCTCCTGCCGGGTGATGGAAAACCCAGCCCGGCCGCCCTGGGCAAG
GCCCTCTGCGCTCTCCTCCTGGCCACTCTCGGCGCCGCGGCCAGCCTCTTGGGGGAGAGTC
CATCTGTTCCGCCAGAGCCCCGGCCAAATACAGCATCACCTTCACGGGCAAGTGGAGCCAGA
CGGCCTTCCCCAAGCAGTACCCCCTGTTCCGCCCCCCTGCGCAGTGGTCTTCGCTGCTGGGG
GCCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAACCAGTACGTAGTAACGGGCTGCG
CGACTTTGCGGAGCGCGGCGAGGCCTGGGCGCTGATGAAGGAGATCGAGGCGGCGGGGGAGG
CGCTGCAGAGCGTGCACGAGGTGTTTTCGGCGCCCGCCGTCCCAGCGGCACCGGGCAGACG
TCGGCGGAGCTGGAGGTGCAGCGCAGGCACTCGCTGGTCTCGTTTGTGGTGCGCATCGTGCC
CAGCCCCGACTGGTTCGTGGGCGTGACAGCCTGGACCTGTGCGACGGGGACCGTTGGCGGG
AACAGGCGGCGCTGGACCTGTACCCCTACGACGCCGGGACGGACAGCGGCTTCACCTTCTCC
TCCCCCAACTTCGCCACCATCCCGCAGGACACGGTGACCGAGATAACGTCCTCCTCTCCCAG
CCACCCGGCCAACTCCTTCTACTACCCGCGGCTGAAGGCCCTGCCTCCCATCGCCAGGGTGA
CACTGCTGCGGCTGCGACAGAGCCCCAGGGCCTTCATCCCTCCCGCCCCAGTCCTGCCCAGC
AGGGACAATGAGATTGTAGACAGCGCCTCAGTTCCAGAAACGCCGCTGGACTGCGAGGTCTC
CCTGTGGTTCGTCTGGGGACTGTGCGGAGGCCACTGTGGGAGGCTCGGGACCAAGAGCAGGA
CTCGCTACGTCCGGGTCCAGCCCCGCAACAACGGGAGCCCCCTGCCCCGAGCTCGAAGAAGAG
GCTGAGTGCGTCCCTGATAACTGCGTCTTAAGACCAGAGCCCCGAGCCCCCTGGGGCCCCCG
GAGCCATGGGGTGTCGGGGGCTCCTGTGCAGGCTCATGCTGCAGGCGGCCGAGGGCACAGGG
GGTTTCGCGCTGCTCCTGACCGCGGTGAGGCCGCGCCGACCATCTCTGCACTGAAGGGCCCT
CTGGTGGCCGGCACGGGCATTGGGAAACAGCCTCCTCCTTTCCCAACCTTGCTTCTTAGGGG
CCCCCGTGTCCCGTCTGCTCTCAGCCTCCTCCTCCTGCAGGATAAAGTCATCCCCAAGGCTC
CAGCTACTCTAAATTATGTCTCCTTATAAGTTATTGCTGCTCCAGGAGATTGTCCTTCATCG
TCCAGGGGCTGGCTCCCACGTGGTTGCAGATACCTCAGACCTGGTGCTCTAGGCTGTGCTG
AGCCCACTCTCCCGAGGGCGCATCCAAGCGGGGGCCACTTGAGAAGTGAATAAATGGGGCGG
TTTCGGAAGCGTCAGTGTTTCCATGTTATGGATCTCTCTGCGTTTGAATAAAGACTATCTCT
GTTGCTCACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

09978187-101501

FIGURE 87

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53971

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35844, pI: 5.45, NX(S/T): 2

MENPSPAAALGKALCALLLATLGAAGQPLGGESIC SARAPAKYSITFTGKWSQTAFPKQYPL
FRPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFAERGEAWALMKEIEAAGEALQSVHEVF
SAPAVPSGTGQTSAELEVQRRHSLVSFVVRIVPSPDWFVGVDSL D L C D G D R W R E Q A A L D L Y P
YDAGTDSGFTFSSPNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLLRLRQSP
RAFIPPAPVLPSRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGR LGTKSRTRYVRVQPA
NNGSPCPELEEEAECVPDNCV

Important features:

Signal peptide:

amino acids 1-26

09978187.101501
TOSTOT.187260

09978187-101501

FIGURE 88

GGCGGCGTCCGTGAGGGGCTCCTTTGGGCAGGGGTAGTGTTTGGTGTCCCTGTCTTGCGTGAT
TATTGACAAACTGAAGCTTTTCTGCACCACTGGACTTAAGGAAGAGTGTACTCGTAGGCGGA
CAGCTTTAGTGCCGGCCGGCCGCTCTCATCCCCGTAAGGAGCAGAGTCCTTTGTACTGAC
CAAGATGAGCAACATCTACATCCAGGAGCCTCCCACGAATGGGAAGGTTTTATTGAAAATA
CAGCTGGAGATATTGACATAGAGTTGTGGTCCAAAGAAGCTCCTAAAGCTTGCAGAAATTTT
ATCCAACCTTTGTTTGGAAGCTTATTATGACAATACCATTTTTTCATAGAGTTGTGCCTGGTTT
CATAGTCCAAGGCGGAGATCCTACTGGCACAGGGAGTGGTGGAGAGTCTATCTATGGAGCGC
CATTCAAAGATGAATTTTATTACGGTTGCGTTTTAATCGGAGAGGACTGGTTGCCATGGCA
AATGCTGGTTCTCATGATAATGGCAGCCAGTTTTTCTTCACTGGGTGAGCAGATGAACT
TAACAATAAGCATACCATCTTTGGAAAGGTTACAGGGGATACAGTATATAACATGTTGCGAC
TGTCAGAAGTAGACATTGATGATGACGAAAGACCACATAATCCACACAAAATAAAAAGCTGT
GAGGTTTTGTTTAAATCCTTTTGATGACATCATTCCAAGGGAAATTAAAAGGCTGAAAAAGA
GAAACCAGAGGAGGAAGTAAAGAAATTGAAACCCAAAGGCACAAAAATTTTAGTTTACTTT
CATTTGGAGAGGAAGCTGAGGAAGAAGAGGAGGAAGTAAATCGAGTTAGTCAGAGCATGAAG
GGCAAAAGCAAAAGTAGTCATGACTTGCTTAAGGATGATCCACATCTCAGTTCTGTTCCAGT
TGTAGAAAGTGAAAAAGGTGATGCACCAGATTTAGTTGATGATGGAGAAGATGAAAGTGCAG
AGCATGATGAATATATTGATGGTGTGATGAAAAGAACCCTGATGAGAGAAAGAATTGCCAAAAA
TTAAAAAAGGACACAAGTGCGAATGTTAAATCAGCTGGAGAAGGAGAAGTGGAGAAGAAATC
AGTCAGCCGCAGTGAAGAGCTCAGAAAAGAAGCAAGACAATTAAAACGGGAACTCTTAGCAG
CAAAACAAAAAAGTAGAAAATGCAGCAAAACAAGCAGAAAAAAGAAGTGAAGAGGAAGAA
GCCCCTCCAGATGGTGTCTGTTGCCGAATACAGAAGAGAAAAGCAAAAGTATGAAGCTTTGAG
GAAGCAACAGTCAAAGAAGGGAACCTCCCGGGAAGATCAGACCCTTGCACTGCTGAACCAGT
TTAAATCTAACTCACTCAAGCAATTGCTGAAACACCTGAAAATGACATTCCTGAAACAGAA
GTAGAAGATGATGAAGGATGGATGTCACATGTACTTCAGTTTGAGGATAAAAGCAGAAAGT
GAAAGATGCAAGCATGCAAGACTCAGATACATTTGAAATCTATGATCCTCGGAATCCAGTGA
ATAAAAGAAGGAGGGAAGAAAGCAAAAAGCTGATGAGAGAGAAAAAAGAAAGAAGATAAAT
GAGAATAATGATAACCAGAACTTGCTGGAAATGTGCCTACAATGGCCTTGTAACAGCCATTG
TTCCCAACAGCATCACTTAGGGGTGTGAAAAGAAGTATTTTTGAACCTGTTGTCTGGTTTTG
AAAAACAATTATCTTGTTTTGCAAATTGTGGAATGATGTAAGCAAATGCTTTTGGTTACTGG
TACATGTGTTTTTTCTAGCTGACCTTTTATATTGCTAAATCTGAAATAAAATAACTTTTCT
TCCACAAAAA

FIGURE 89

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50919

><subunit 1 of 1, 472 aa, 1 stop

><MW: 53847, pI: 5.75, NX(S/T): 2

MSNIYIQEPPTNGKVLLKTTAGDIDIELWSKEAPKACRNFIQLCLEAYYDNTIFHRVVPGFI
VQGGDPTGTGSGGESIYGAPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQFFFTLGRADELN
NKHTIFGKVTGDTVYNMLRLSEVDIDDDERPHNPHKIKSCEVLFPFDDIIPREIKRLKKEK
PEEEVKKLKPKGTKNFSLLSFGEAEEEEEEEVNVRVSQSMKGKSKSSHDLKDDPHLSSVPVV
ESEKGDAPDLVDDGEDESAEHDEYIDGDEKNLMRERIAKKLKKDTSANVKSAGEGEVEKKSV
SRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEEAPPDGAVAEYRREKQKYEALRK
QQSKKGTSREDQTLALLNQFKSKLTQAIAETPENDIPETEVEDDEGWMSHVLQFEDKSRKVK
DASMQSDTFEIIDPRNPVNKRREESKKLMREKKERR

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 109-112 and 201-204

Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.

amino acids 49-66

Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase

amino acids 96-140, 49-89 and 22-51

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TOSTOT-EST-660

FIGURE 90

CGCCGCCGTTGGGGCTGGAAGTTCCCGCCAGGTCCGTGCCGGGCGAGAGAGATGCTGCCCGG
 CCCGCCTCGGCTTTGAGGCGAGAGAAGTGTCCAGACCCATTTTCGCCTTGCTGACGGCGTCTG
 AGCCCTGGCCAGACATGTCCACAGGGTTCTCCTTCGGGTCCGGGACTCTGGGCTCCACCACC
 GTGGCCGCCGGCGGGACCAGCACAGGCGGCGTTTTCTCCTTCGGAACGGGAACGTCTAGCAA
 CCCTTCTGTGGGGCTCAATTTTGGAATCTTGGAAGTACTTCAACTCCAGCAACTACATCTG
 CTCCTTCAAGTGGTTTTTGGAACCGGGCTCTTTGGATCTAAACCTGCCACTGGGTTCACTCTA
 GGAGGAACAAATACAGGTGCCTTGCACACCAAGAGGCCTCAAGTGGTCACCAAATATGGAAC
 CCTGCAAGGAAAACAGATGCATGTGGGGAAGACACCCATCCAAGTCTTTTTAGGAGTCCCCT
 TCTCCAGACCTCCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCCGGAGCCCTGGAAA
 GGAATCAGAGATGCTACCACCTACCCGCCTGGATGGAGTCTCGCTCTGTGCGCCAGGCTGGAG
 TGCAGTGGCACGATCTCGGCTCACTGCAACCTCCGCCTCCCGGGTTCAAGCGAGTCTCCTGC
 CTCAGCCTCTGAGTGTCTGGGGCTACAGGTGCCTGCAGGAGTCTGGGGCCAGCTGGCCTCG
 ATGTACGTGAGCACGCGGGAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTCTGTACCT
 GAACGTGTACGCGCCGGCGCGCGCGCCCGGGGATCCCCAGCTGCCAGTGATGGTCTGGTTCC
 CGGGAGGCGCCTTCATCGTGGGCGCTGCTTCTTCGTACGAGGGCTCTGACTTGGCCGCCCGC
 GAGAAAGTGGTGTGGTGTCTTCTGCAGCACAGGCTCGGCATCTTCGGCTTCCTGAGCACGGA
 CGACAGCCACGCGCGCGGGAACCTGGGGGCTGCTGGACCAGATGGCGGCTCTGCGCTGGGTGC
 AGGAGAACATCGCAGCCTTCGGGGGAGACCCAGGAAATGTGACCCTGTTCCGCCAGTCGGCG
 GGGGCCATGAGCATCTCAGGACTGATGATGTACCCCTAGCCTCGGGTCTCTTCCATCGGGC
 CATTTCCAGAGTGGCACCGCGTTATTTCAGACTTTTCATCACTAGTAACCCACTGAAAGTGG
 CCAAGAAGGTTGCCACCTGGCTGGATGCAACCACAACAGCACACAGATCCTGGTAAACTGC
 CTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGATGAGATTCTCCAACCT
 GAACTTCCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGG
 TGATCCCAGATGACCCTTTGGTGCTCCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTT
 CTAGGTGTCAACAACCTGGAATTCAATTGGCTCTTGCCCTTATAATATCACCAAGGAGCAGGT
 ACCACTTGTGGTGGAGGAGTACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAA
 ACCGTATGATGGACATAGTTCAAGATGCCACTTTCGTGTATGCCCACTGCAGACTGCTCAC
 TACCACCGAGAAACCCCAATGATGGGAATCTGCCCTGCTGGCCACGCTACAACAAGGATGAA
 AAGTACCTGCAGCTGGATTTTACCACAAGAGTGGGCATGAAGCTCAAGGAGAAGAAGATGGC
 TTTTTGGATGAGTCTGTACCAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGC
 TATGCAGGAAGGAGCCAAAGAGGGGTTTGCCCCCACCATCCAGGCCCTGGGGAGACTAGCCA
 TGGACATACCTGGGGACAAGAGTTCTACCCACCCAGTTTAGAACTGCAGGAGCTCCCTGCT
 GCCTCCAGGCCAAAGCTAGAGCTTTTGCCCTGTTGTGTGGGACCTGCACTGCCCTTTCCAGCC
 TGACATCCCATGATGCCCTCTACTTCACTGTTGACATCCAGTTAGGCCAGGCCCTGTCAAC
 ACCACACTGTGCTCAGCTCTCCAGCCTCAGGACAACCTCTTTTTTTCCCTTCTTCAAATCCT
 CCCACCCTTCAATGTCTCCTTGTGACTCCTTCTTATGGGAGGTGACCCAGACTGCCACTGC
 CCCTGTCACTGCACCCAGCTTGGCATTTACCATCCATCCTGCTCAACCTTGTTCCCTGTCTGT
 TCACATTGGCCTGGAGGCCTAGGGCAGGTTGTGACATGGAGCAAACCTTTTGGTAGTTTGGGA
 TCTTCTCTCCACCCACACTTATCTCCCCAGGGCCACTCCAAAGTCTATACACAGGGGTGG
 TCTCTTCAATAAAGAAGTGTTGATTAGAAAAA

FIGURE 91

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44179

<subunit 1 of 1, 545 aa, 1 stop

<MW: 58934, pI: 9.45, NX(S/T): 4

MSTGFSFGSGTLGSTTVAAGGTSTGGVFSFGTGTSSNPSVGLNFGNLGSTSTPATTAPSSG
FGTGLFGSKPATGFTLGGTNTGALHTKRPQVVTKYGT LQ GKQMHVGKTPIQVFLGVPF SRPP
LGILRFAPPEPPEPWKGIRDATTYPGW\$ LALSPGWSAVARSRLTATSASRVQASLLPQPLS
VWGYRCLQESWGQLASMYVSTRERYKWLRFSEDCLYLNVYAPARAPGDPQLPVMVWFPGGAF
IVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLLDQMAALRWVQENIA
AFGGDPGNVT LFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVA
HLAGCNHNSTQILVNCLRALSGTKVMRVS NKMRF LQLNFQ RDPEEIIWSMSPVVDGVVIPDD
PLVLLTQGKVSSVPYLLGVNNLEFNWLLPYNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMMD
IVQDATFVYATLQTAHYHRET PMMGICPAGHATTRMKSTCSWILPQEWA

Important features:

Signal peptide:

amino acids 1-29

Carboxylesterases type-B serine active site.

amino acids 312-327

Carboxylesterases type-B signature 2.

amino acids 218-228

N-glycosylation sites.

amino acids 318-321, 380-383 and 465-468

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TOSTOT 497660

FIGURE 92

GAGAACAGGCCTGTCTCAGGCAGGCCCTGCGCCTCCTATGCGGAGATGCTACTGCCACTGCT
GCTGTCCTCGCTGCTGGGCGGGTCCCAGGCTATGGATGGGAGATTCTGGATACGAGTGCAGG
AGTCAGTGATGGTGCCGAGGGCCTGTGCATCTCTGTGCCCTGCTCTTTCTCCTACCCCCGA
CAAGACTGGACAGGGTCTACCCCAGCTTATGGCTACTGGTTCAAAGCAGTGACTGAGACAAC
CAAGGGTGCTCCTGTGGCCACAAACCACCAGAGTCGAGAGGTGGAAATGAGCACCCGGGGCC
GATTCAGCTCACTGGGGATCCCGCCAAGGGGAAGTCTCCTTGGTGATCAGAGACGCGCAG
ATGCAGGATGAGTCACAGTACTTCTTTCTGGGTGGAGAGAGGAAGCTATGTGACATATAATTT
CATGAACGATGGGTCTTTCTAAAAGTAACAGTGCTCAGCTTCACGCCCAGACCCCAGGACC
ACAACACCGACCTCACCTGCCATGTGGACTTCTCCAGAAAGGGTGTGAGCGCACAGAGGACC
GTCCGACTCCGTGTGGCCTATGCCCCCAGAGACCTTGTATCAGCATTTACGTGACAACAC
GCCAGCCCTGGAGCCCCAGCCCCAGGGAAATGTCCCATACCTGGAAGCCCCAAAAGGCCAGT
TCCTGCGGCTCCTCTGTGCTGCTGACAGCCAGCCCCCTGCCACACTGAGCTGGGTCTGCGAG
AACAGAGTCCTCTCCTCGTCCCATCCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGG
GGTGAAGGCTGGGGATTGAGGGCGCTACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGC
AGCGAGCCCTGGACCTCTCTGTGCAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAA
GCAAACAGGACAGTCCTGGAAAACCTTGGGAACGGCACGTCTCTCCAGTACTGGAGGGCCA
AAGCCTGTGCCTGGTCTGTGTACACACAGCAGCCCCCAGCCAGGCTGAGCTGGACCCAGA
GGGGACAGGTTCTGAGCCCCCTCCAGCCCTCAGACCCCGGGGTCTGGAGCTGCCTCGGGTT
CAAGTGAGCACGAAGGAGAGTTACCTGCCACGCTCGGCACCCACTGGGCTCCCAGCACGT
CTCTCTCAGCCTCTCCGTGCACTATAAGAAGGGACTCATCTCAACGGCATTCTCCAACGGAG
CGTTTCTGGGAATCGGCATCACGGCTCTTCTTTTCTCTGCTGGCCCTGATCATCATGAAG
ATTCTACCGAAGAGACGGACTCAGACAGAAACCCGAGGCCAGGTTCTCCCGGCACAGCAC
GATCCTGGATTACATCAATGTGGTCCCGACGGCTGGCCCCCTGGCTCAGAAGCGGAATCAGA
AAGCCACACCAAACAGTCCTCGGACCCCTCCTCCACCAGGTGCTCCCTCCCAGAATCAAAG
AAGAACCAGAAAAAGCAGTATCAGTTGCCAGTTTCCAGAACCCAAATCATCCACTCAAGC
CCCAGAATCCCAGGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCA
GACCCAGGCCTGAGGCCCGGATGCCCAAGGGCACCCAGGCGGATTATGCAGAAGTCAAGTTC
CAATGAGGGTCTCTTAGGCTTTAGGACTGGGACTTCGGCTAGGGAGGAAGGTAGAGTAAGAG
GTTGAAGATAACAGAGTGCAAAGTTTCTTCTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCT
CTCTCTTTCTCTCTCTTTTAAAAAAACATCTGGCCAGGGCACAGTGGCTCACGCCTGTAATC
CCAGCACTTTGGGAGGTTGAGGTGGGCAGATCGCCTGAGGTGCGGAGTTCGAGACCAGCCTG
GCCAACTTGGTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCTGGGCATGGTGGCAGG
CGCCTGTAATCCTACCTACTTGGGAAGCTGAGGCAGGAGAATCACTTGAACCTGGGAGACGG
AGGTTGCAGTGAGCCAAGATCACACCATTGCACGCCAGCCTGGGCAACAAAGCGAGACTCCA
TCTCAAAAAAAAAAATCCTCCAAATGGGTGGGTGTCTGTAATCCAGCACTTTGGGAGGCTA
AGGTGGGTGGATTGCTTGAGCCCAGGAGTTCGAGACCAGCCTGGGCAACATGGTGAAACCCC
ATCTCTACAAAAAATACAAAACATAGCTGGGCTTGGTGGTGTGTGCCTGTAGTCCCAGCTGT
CAGACATTTAAACCAGAGCAACTCCATCTGGAATAGGAGCTGAATAAAATGAGGCTGAGACC
TACTGGGCTGCATTCTCAGACAGTGGAGGCATTCTAAGTCACAGGATGAGACAGGAGGTCCG
TACAAGATACAGGTCATAAAGACTTTGCTGATAAAACAGATTGCAGTAAAGAAGCCAACCAA
ATCCCACCAAAACCAAGTTGGCCACGAGAGTGACCTCTGGTCGTCTCTCACTGCTACACTCCT
GACAGCACCATGACAGTTTACAAATGCCATGGCAACATCAGGAAGTTACCCGATATGTCCCA
AAAGGGGGAGGAATGAATAATCCACCCCTTGTTTAGCAAATAAGCAAGAAATAACCATAAAA
GTGGGCAACCAGCAGCTCTAGGCGCTGCTCTTGTCTATGGAGTAGCCATTCTTTTGTTCCTT
TACTTTCTTAATAAACTTGCTTTACCTTAAAAAAA

FIGURE 93

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA54002

><subunit 1 of 1, 544 aa, 1 stop

><MW: 60268, pI: 9.53, NX(S/T): 3

MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYWFK
AVTETTKGAPVATNHQSREVEEMSTRGRFQLTGDPKGNCSLVIRDAQMQDESQYFFRVERGS
YVTYNFMNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVIS
ISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHPWGPRPL
GLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLENLGNGTSL
PVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQSPDPGVLELPRVQVEHEGEFTCHARHP
LGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPR
FSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPPPPGAPSPESKKNQKKQYQLPSFPEP
KSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ

Important features:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 100-103, 297-300 and 306-309

Immunoglobulins and major histocompatibility complex proteins signature.

amino acids 365-371

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FIGURE 94

TGAAGAGTAATAGTTGGAATCAAAAGAGTCAACGCAATGAAGTGTATTACTGCTGCGTTT
TATGTTGGGAATTCCTCTCCTATGGCCTTGTCTTGAGCAACAGAAAACCTCTCAAACAAAGA
AAGTCAAGCAGCCAGTGCGATCTCATTGAGAGTGAAGCGTGGCTGGGTGTGGAACCAATTT
TTTGTACCAGAGGAAATGAATACGACTAGTCATCACATCGGCCAGCTAAGATCTGATTTAGA
CAATGGAAACAATTTCTTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAGTACTTTTATCA
TTGATGAAAGAACAGGTGACATATATGCCATACAGAAGCTTGATAGAGAGGAGCGATCCCTC
TACATCTTAAGAGCCCAGGTAATAGACATCGCTACTGGAAGGGCTGTGGAACCTGAGTCTGA
GTTTGTTCATCAAAGTTTCGGATATCAATGACAATGAACCAAAATTCCTAGATGAACCTTATG
AGGCCATTGTACCAGAGATGTCTCCAGAAGGAACATTAGTTATCCAGGTGACAGCAAGTGAT
GCTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCCTCTACAGCTTACTTCAAGGCCAGCC
ATATTTTTCTGTTGAACCAACAACAGGAGTCATAAGAATATCTTCTAAAATGGATAGAGAAC
TGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTG
TCTGGAACAACAAGTGTATTAATTAACCTTTCAGATGTTAATGACAATAAGCCTATATTTAA
AGAAAGTTTATACCGCTTGACTGTCTCTGAATCTGCACCCACTGGGACTTCTATAGGAACAA
TCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTACAGCATTGAAGAGGAT
GATTTCGCAAACATTTGACATTATTACTAATCATGAACTCAAGAAGGAATAGTTATATTTAA
AAAGAAAGTGGATTTTGAGCACCAGAACCACTACGGTATTAGAGCAAAAGTTAAAAACCATC
ATGTTCCCTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCCTTTCATTAAGATCCAG
GTGGAAGATGTTGATGAGCCTCCTCTTTTCTCCTTCCATATTATGTATTTGAAGTTTTTGA
AGAAACCCACAGGGATCATTTGTAGGCGTGGTGTCTGCCACAGACCCAGACAATAGGAAAT
CTCCTATCAGGTATTCTATTACTAGGAGCAAAGTGTTCATATCAATGATAATGGTACAATC
ACTACAAGTAACTCACTGGATCGTGAAATCAGTGCTTGGTACAACCTAAGTATTACAGCCAC
AGAAAAATACAATATAGAACAGATCTCTTCGATCCCCTGTATGTGCAAGTTCTTAACATCA
ATGATCATGCTCCTGAGTTCTCTCAATACTATGAGACTTATGTTTGTGAAAATGCAGGCTCT
GGTCAGGTAATTCAGACTATCAGTGCAGTGGATAGAGATGAATCCATAGAAGAGCACCATTT
TTACTTTAATCTATCTGTAGAAGACACTAACAAATTCAGTTTTACAATCATAGATAATCAAG
ATAACACAGCTGTCAATTTGACTAATAGAACTGGTTTTAACCTTCAAGAAGAACCTGTCTTC
TACATCTCCATCTTAATTGCCGACAATGGAATCCCGTCACTTACAAGTACAAACACCCTTAC
CATCCATGTCTGTGACTGTGGTGACAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTG
TGCTTTCCATGGGATTCAAGACAGAAGTTATCATTGCTATTCTCATTGTCATTATGATCATA
TTTGGGTTTATTTTTTTGACTTTGGGTTTAAACAACGGAGAAAACAGATTCTATTTCTCTGA
GAAAAGTGAAGATTTTCAAGAGAGAATATATTCCAATATGATGATGAAGGGGGTGGAGAAGAAG
ATACAGAGGCCTTTGATATAGCAGAGCTGAGGAGTAGTACCATAATGCGGGAACGCAAGACT
CGGAAAACCACAAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTTGGCCCCGA
CAGTGCCATATTCAGGAAATTCATTCTGGAAGCTCGAAGAAGCTAATACTGATCCGTGTG
CCCCCTCTTTTGATTCCCTCCAGACCTACGCTTTTGAGGGAACAGGGTCATTAGCTGGATCC
CTGAGCTCCTTAGAATCAGCAGTCTCTGATCAGGATGAAAGCTATGATTACCTTAATGAGTT
GGGACCTCGCTTTAAAAGATTAGCATGCATGTTTGGTTCTGCAGTGCAGTCAAATAATTAGG
GCTTTTTTACCATCAAAATTTTTTAAAAGTGCTAATGTGTATTTCGAACCCAATGGTAGTCTTAA
AGAGTTTTGTGCCCTGGCTCTATGGCGGGGAAAGCCCTAGTCTATGGAGTTTTCTGATTTCC
CTGGAGTAAATACTCCATGGTTATTTTTAAGCTACCTACATGCTGTCTATTGAACAGAGATGTG
GGGAGAAATGTAAACAATCAGCTCACAGGCATCAATAACAACCAGATTTGAAGTAAATAATG
TAGGAAGATATTAAAAGTAGATGAGAGGACACAAGATGTAGTCGATCCTTATGCGATTATAT
CATTATTTACTTAGGAAAGAGTAAAAATACCAAACGAGAAAATTTAAAGGAGCAAAAATTTG
CAAGTCAAATAGAAATGTACAAATCGAGATAACATTTACATTTCTATCATATTGACATGAAA
ATTGAAAATGTATAGTCAGAGAAATTTTCATGAATTATTCATGAAGTATTGTTTCCTTTAT
TTAAA

FIGURE 95

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906

><subunit 1 of 1, 772 aa, 1 stop

><MW: 87002, pI: 4.64, NX(S/T): 8

MNCYLLLRFMLGIPLLPCLGATENSQTKKVKQPVRSHLRVKRGWVWNQFFVPEEMNTTSHH
IGQLRSDLDNGNNSFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIAT
GRAVEPESEFVIKVS DINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTASDADDPSSGNNARL
LYSLLQGQPYFSVEPTTG VIRISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLS D
VNDNKPIFKESLYRLTVSESAPTGT SIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHE
TQEGIVILKKKVD FEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLL
PYYVFEVFEETPQGSFVGVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISA
WYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDR
DESIEEHFHYFNLSVEDTNNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIP
SLTSTNTLTIIHVCD CGDSGSTQTCQYQELVLSMGFKTEVIIAILICIMIIFGFIFLTGLKQ
RRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLY
RQSLQVGPD SAIFRKFILEKLEEANTDPCAPPFD SLQTYAFEGTGSLAGSLSSLES AVSDQD
ESYDYLNELGPRFKRLACMFGSAVQSNN

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 597-617

N-glycosylation sites.

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518,
516-519 and 534-537

Cadherins extracellular repeated domain signature.

amino acids 136-146 and 244-254

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FIGURE 96

ATTTCAAGGCCAGCCATATTTTTNTGTTGAACCAACAACAGGAGTCATAAGAATATTTTNTA
AAATGGATAGAGAACTGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGT
CAGCCAGGAGCGTTGTNTGGAACAACAAGTGTATTAATTAACTTTCAGATGTTAATGACAA
TAAGCCTATATTTAAAGAAAGTTTATACCGCTTGACTGTNTNTGAATCTGCACCCACTGGGA
NTTNTATAGGAACAATCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTAC
AGCATTGAAGAGGATGATTTCGCAAACATTTGACATTATT

09078187-101501

FIGURE 97

GCAACCTCAGCTTCTAGTATCCAGACTCCAGCGCCGCCCGGGCGCGGACCCCAACCCCGAC
CCAGAGCTTCTCCAGCGGCGGGCGCAGCGAGCAGGGCTCCCCGCCTTAACCTCCTCCGCGGGG
CCCAGCCACCTTTCGGGAGTCCGGGTGCCCCACCTGCAAACCTCTCCGCCTTCTGCACCTGCCA
CCCCTGAGCCAGCGCGGGCCCCCGAGCGAGTCAATGGCCAACGCGGGGCTGCAGCTGTTGGGC
TTCATTCTCGCCTTCTGCGGATGGATCGGCGCCATCGTCAGCACTGCCCTGCCCCAGTGAG
GATTTACTCCTATGCCGGCGACAACATCGTGACCGCCAGGCCATGTACGAGGGGCTGTGGA
TGTCTGCGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAAT
CTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGAT
AGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGC
AGAAGATGAGGATGGCTGTCAATTGGGGGTGCGATATTTCTTCTTGCAAGTCTGGCTATTTTA
GTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCTATGACCCAGT
CAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCC
TTCTGGGAGGTGCCCTACTTTGCTGTTCTGTCCCCGAAAAACAACCTCTTACCCAACACCA
AGGCCCTATCCAAAACCTGCACCTTCCAGCGGGAAAGACTACGTGTGACACAGAGGCAAAAG
GAGAAAATCATGTTGAAACAAACCGAAAATGGACATTGAGATACTATCATTAACATTAGGAC
CTTAGAATTTTGGGTATTGTAATCTGAAGTATGGTATTACAAAACAAACAAACAAAAA
ACCCATGTGTTAAATACTCAGTGCTAAACATGGCTTAATCTTATTTTATCTTCTTCTCTCA
ATATAGGAGGGAAGATTTTCCATTTGTATTACTGCTTCCCATTGAGTAATCATACTCAAAT
GGGGGAAGGGGTGCTCCTTAAATATATATAGATATGTATATATACATGTTTTTCTATTA
ATAGACAGTAAAATACTATTCTCATTATGTTGATACTAGCATACTTAAAATATCTCTAAAT
AGGTAAATGTATTTAATTCCATATTGATGAAGATGTTTATTGGTATATTTTCTTTTCTGTC
TTATATACATATGTAACAGTCAAATATCATTACTCTTCTTCACTAGCTTTGGGTGCCTTTG
CCACAAGACCTAGCCTAATTTACCAAGGATGAATTCTTTCAATTCTTCATGCGTGCCCTTTT
CATATACTTATTTTATTTTTTACCATAATCTTATAGCACTTGCAATCGTTATTAAGCCCTTAT
TTGTTTTGTGTTTCATTGGTCTCTATCTCCTGAATCTAACACATTTTCATAGCCTACATTTTA
GTTTCTAAAGCCAAGAAGAATTTATTACAAATCAGAACTTTGGAGGCAAATCTTTCTGCATG
ACCAAAGTGATAAATTCCTGTTGACCTTCCCACACAATCCCTGTACTCTGACCCATAGCACT
CTTGTTTGCTTTGAAAATATTTGTCCAATTGAGTAGCTGCATGCTGTTCCCCCAGGTGTTGT
AACACAACCTTTATTGATTGAATTTTAAAGCTACTTATTATAGTTTTATATCCCCCTAACT
ACCTTTTTGTTCCCCATTCCTTAATTGTATTGTTTTCCCAAGTGTAATTATCATGCGTTTTA
TATCTTCCTAATAAGGTGTGGTCTGTTTGTCTGAACAAAGTGCTAGACTTTCTGGAGTGATA
ATCTGGTGACAAATATTCTCTCTGTAGCTGTAAGCAAGTCACTTAATCTTTCTACCTCTTTT
TTCTATCTGCCAAATTGAGATAATGATACTTAACCAGTTAGAAGAGGTAGTGTGAATATTAA
TTAGTTTATATTACTCTTATTCTTTGAACATGAACATATGCCTATGTAGTGTCTTTATTTGCT
CAGCTGGCTGAGACACTGAAGAAGTCACTGAACAAAACCTACACACGTACCTTCATGTGATT
CACTGCCTTCCTCTCTCTACCAGTCTATTTCCACTGAACAAAACCTACACACATACCTTCAT
GTGGTTCAGTGCCTTCCTCTCTCTACCAGTCTATTTCCACTGAACAAAACCTACGCACATAC
CTTCATGTGGCTCAGTGCCTTCCTCTCTCTACCAGTCTATTTCCATTCTTTAGCTGTGTCT
GACATGTTTGTGCTCTGTTCCATTTTAAACAACCTGCTCTTACTTTTCCAGTCTGTACAGAATG
CTATTTCACTTGAGCAAGATGATGTAATGGAAAGGGTGTGGCACTGGTGTCTGGAGACCTG
GATTTGAGTCTTGGTGCTATCAATCACCGTCTGTGTTTGAGCAAGGCATTTGGCTGCTGTAA
GCTTATTGCTTCATCTGTAAGCGGTGGTTTGTAATTCCTGATCTTCCCACCTCACAGTGATG
TTGTGGGGATCCAGTGAGATAGAATACATGTAAGTGTGGTTTTGTAATTTAAAAAGTGCTAT
ACTAAGGGAAAGAATTGAGGAATTAAGTGCATACGTTTTGGTGTTGCTTTTCAAATGTTTGA
AAATAAAAAAATGTTAAG

FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185

><subunit 1 of 1, 211 aa, 1 stop

><MW: 22744, pI: 8.51, NX(S/T): 1

MANAGLQLLGFI LAFLGWIGAI VSTALPQWRIYSYAGDNIVTAQAMY EGLWMSCVSQSTGQI
QCKVFDSLNLNLSSTLQATRALMVVGILLGVIAIFVATVGMKCMKCLEDDEVQKMRMAVIGGA
IFLLAGLAILVATAWYGNRIVQEFYDPMTPV NARYEFGQALFTGWAAASLCLLGALLCCSC
PRKTTSYPTPRPYPKPAPSSGKDYV

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-102, 118-142 and 161-187

N-glycosylation site.

amino acids 72-75

PMP-22 / EMP / MP20 family proteins

amino acids 70-111

ABC-2 type transport system integral membrane protein

amino acids 119-133

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FIGURE 99

TTCTGGCCAAACCCGGGGCTNCAGCTGTTGGGCTTCATCTCGCCTTCCTGGGATGGATCGGC
GCCATCNTCACACTGCCCTTCCCCAGTGGAGGATTTTACTCCCTATGCTGGCGACAACATCG
TGACCGCCCAGCCCATGTACGAGGGGCTGTGGATGTCCNGCGTGTGCGAGAGCACCGGGCAG
ATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCCGTGC
CTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGA
AGTGTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGC
GCGATATTTCTTCTTGCAAGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAAN
CNTTCAACANTTCTATGACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCA
GGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCT
GTTCTGTCCC

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FIGURE 100

ACCCTTGACCCAACGCGGCCCCCGACCGNTTCATGGCCAAACGCGGGNCTCCAGCTGTTGG
GCTTCATTCTCCCCCTTCCTGGGATGGACCGGCGCCCATCNTCAGCACTGCCCTGCCCCAGTG
GAGGATTTACTCCTATNCCGGCNACAACATCGTGACCGCCCAGGCCNTGTACGAGGGGCTGT
GGATGTCCTGCGTGTCGCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCCTTGCT
GAATCTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGTGGTTGGCATCCTCCTGGGAG
TGATAGCAATCTTNNTGGCCACCGTTGTNNNTGAAGTGTATGAAGTGCTTGGAAGACGATGA
GGTGCAGAAGATGAGGATGGCTGTCAATTGGGGGCGCGATATTTCTTCTTGACAGGTCTGGCTA
TTTTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCTATGACCGA

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FIGURE 101

GGGCCCCGACCATTATCCAACCGGGNTCACTGTTGGCTCATCTCCCTCCTGGATGAANCGCGC
CATCNTCAGACTCCCTGCCCCATGGAGATTTNNCCTATGCTGGCGACAACATCNTGACCCCC
AGCCATGTACGAGGGGCTTTGAACGTCNGCGTGTGCGAGANCACCGGGCAGATCCAGTGCAA
AGTCTTTGACTCCTTGCTGAATCTGNGCAGCACATTGCAGCAACCCNTGCCCTGATGGTGGT
TGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGT
GCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTT
CTTGCAGGTCTGGCTATTTNNNGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAAT
TCTATGACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGC
TGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTCTCCTGCGA

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FIGURE 102

ATTCTCCCCTCCTGGATGGATCGCNCCACCGTCACATTGCCTTCCCCCANTGGAGGATTNAC
TCCTATGCTGGCGACAACATCGTGACCCCCCAGGCCATTTACCGAGGGGCTTTGGATGTCNT
GCNTGTCGCAGAGCACCGGGCAGATCCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAG
CAGCACATTGCAAGCAACCCGTGCCTTGATGGGGTTGGCATCCTCCTGGGAGTGATAGCAAC
CTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGCCAGAAG
ATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTGTTGCAGGTCTGGCTATTTTAGTNGC
CACAGCATGGTATGGCAATAGANTNNTTCNNGNNNTCTATGACCCTATGACCCCAGTCAATG
CCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTG
GGAGGTGCCCTACTTTGCTGTTCCCTGTCCC

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FIGURE 103

AGAGCACCGGCAGATCCCAGTNCAAAGTCTTTGACCCTTGCTGAATCTGAGCAGCACATTNC
AAGCAACCCCTTGCCTTGAAGGTGGTTGNCATCCCCCCTGGGAGTGAATAGCAATCTTTGTG
GCCACCGTTGGCATGAAGTNTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGAT
GGCTGTCATTGGGGGCGCGATATTTCTTCTTGCAAGTCTGGCTATTTTAGTNNCCACAGCAT
GGTATGGCAATAGNATNNTTCGNGGNTTCTATGACCCTATGACCCCACTCAATGCCAGGTAC
GAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGC
CCTACTTTGCTGTTCTGTCCCCGAA

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FIGURE 104

AGCAATGCCCTGCCCCCAGTGGAGGATTAATTCCTATGNTGGGGACAACATTGTGACNGCCC
AGGCCATGTACGGGGGGCTGTGGATGTCCTGCGTGTCGCAGAGCACCGGGCAGATCCAGTGC
AAAGTNTTTGACTCCTTGCTGAATTTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGT
GGTTGGCATCTTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTGGNAATGAAGTGTATGA
AGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTT
CTTNTTGCAGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAATNGTTCAAGA
ATTTTATGACCCTATGACCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTTTNTTCACTG
GCTGGGCTGCTGCTTNTTTCTGCCTTNTGGGAGGTGCCCTANTTTGCTGTTCTGCGAACC

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FIGURE 105

TCATAGGGGGGCGCGATATTTTTCTTGCAGGTNTGGTTATTTTAGTTGCCACAGCATGGTA
TGGCAATAGAATCGTTCAAGAATTNTATGACCCTATGACCCCAGTCAATGCCAGGTACGAAT
TTGGTCAGGCTCTNTTCACTGGNTGGGCTGCTGCTTCTNTNNGCCTTNTGGGAGGTGCCCTA
CTTTGCTGTTCTG

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FIGURE 106

TTCCTGGGATGGATCCGCCCCATCNTCACATGCCCTGCCCCNTGGAGATTTACNCCTATGC
TGGCGAACAAACATCNTGACCGCCCAGGCCATGTACGAGGGGCTGTGGAATGTCCTGCGTGTC
CCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACAT
TGCAAGCAACCNTGCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGG
CCACCGTTGGCATGAAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGAT
GGCTGTCAATTGGGGGCGCGATATTTCTTCTTGCAAGTCTGGCTATTTTAGNNGCCACAGCAT
GGTATGGCAATCAGACCCNNTCANAACTCTATGACCCTATGACCCCAAGTCAATGCCAGGTA
CGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTG
CCCTACTTTGCTGTTCTGTCCCCGAAAAACAACCTCTTACCCACG

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FIGURE 107

CGGGGCTGCAGCTGTTGGGCTTCATCTCGCTTCCTGGGATGGAATCGGCGCCATCGTCAGCA
CTGCCCTGCCCCATGGAGGATTTACTCNTATGCTGGCGACAACATCGTGACCNCCCAGGCCA
TGTACGAGGGGCTGTGGATGTCNGCGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCT
TTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCNTGCCTTGATGGTGGTTGGCA
TCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTG
GAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTCTTGC
AGGTCTGGCTATTTNTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTAT
GACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGC
TGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTCTCCTGCGAA

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FIGURE 108

CGGTGCCGTCAGCTCGCCGGGCACCGCGGCCTCGCCCTCGCCCTCCGCCCCCTGCGCCTGCAC
CGCGTAGACCGACCCCCCTCCAGCGCGCCACCCGGTAGAGGACCCCCGCCCCGTGCCCCG
ACCGGTCCCCGCCTTTTTGTAAACTTAAAGCGGGCGCAGCATTAAACGCTTCCCGCCCCGGT
GACCTCTCAGGGGTCTCCCCGCCAAAGGTGCTCCGCCGCTAAGGAACATGGCGAAGGTGGAG
CAGGTCCTGAGCCTCGAGCCGCAGCACGAGCTCAAATTCGAGGTCCCTTCACCGATGTTGT
CACCACCAACCTAAAGCTTGGCAACCCGACAGACCGAAATGTGTGTTTTAAGGTGAAGACTA
CAGCACCACGTAGGTACTGTGTGAGGCCCAACAGCGGAATCATCGATGCAGGGGCCTCAATT
AATGTATCTGTGATGTTACAGCCTTTTCGATTATGATCCCAATGAGAAAAGTAAACACAAGTT
TATGGTTCAGTCTATGTTTGTCTCCAAGTACACTTCAGATATGGAAGCAGTATGGAAGGAGG
CAAAACCGGAAGACCTTATGGATTCAAACTTAGATGTGTGTTTGAATTGCCAGCAGAGAAT
GATAAACCACATGATGTAGAAATAAAATAAATTATATCCACAAGTGCATCAAAGACAGAAAC
ACCAATAGTGTCTAAGTCTCTGAGTTCCTCTTTGGATGACACCGAAGTTAAGAAGGTTATGG
AAGAATGTAAGAGGCTGCAAGGTGAAGTTCAGAGGCTACGGGAGGAGAACAAAGCAGTTCAAG
GAAGAAGATGGACTGCGGATGAGGAAGACAGTGCAGAGCAACAGCCCCATTTTCAGCATTAGC
CCCAACTGGGAAGGAAGAAGGCCTTAGCACCCGGCTCTTGGCTCTGGTGGTTTTGTCTTTA
TCGTTGGTGTAAATTATTGGGAAGATTGCCTTGTAGAGGTAGCATGCACAGGATGGTAAATTG
GATTGGTGGATCCACCATATCATGGGATTTAAATTTATCATAACCATGTGTAAAAAGAAATT
AATGTATGATGACATCTCACAGGTCTTGCCTTTAAATTACCCCTCCCTGCACACACATACAC
AGATACACACACACAAATATAATGTAACGATCTTTTAGAAAGTTAAAAATGTATAGTAACTG
ATTGAGGGGGAAAAAGAATGATCTTTATTAATGACAAGGGAAACCATGAGTAATGCCACAAT
GGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCTTGGTACATGATGCTGGATTACCTC
TCTTAAATGACACCCTTCCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTGGAGCCCAGCAT
GCTGGGGAGTGCGGTGAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCCAGGCTG
CTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGA
AGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAAGGCGTGTGT
TGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAA
GCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACCTGTTATTTCAGAGATGTTTAAATGCATA
TTTAACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAATGC
TGCGTGCTGCTGAACTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTGTGGGCTCCTCT
GTCTCTGGAGAGTCTGGTCATGTGGAGGTGGGGTTTTATTGGGATGCTGGAGAAGAGCTGCCA
GGAAGTGTTTTTTCTGGGTGAGTAAATAACAACTGTCATAGGGAGGGAAATTCTCAGTAGTG
ACAGTCAACTCTAGGTTACCTTTTTTAAATGAAGAGTAGTCAGTCTTCTAGATTGTTCTTATA
CCACCTCTCAACCATTACTCACACTTCCAGCGCCAGGTCCAAGTCTGAGCCTGACCTCCCC
TTGGGGACCTAGCCTGGAGTCAGGACAAATGGATCGGGCTGCAGAGGGTTAGAAGCGAGGGC
ACCAGCAGTTGTGGGTGGGGAGCAAGGGAAGAGAGAACTCTTCAGCGAATCCTTCTAGTAC
TAGTTGAGAGTTTGAAGTGTGAATTAATTTTATGCCATAAAAGACCAACCAGTTCTGTTTGA
CTATGTAGCATCTTGAAAAGAAAAATTATAATAAAGCCCCAAAATTAAGAAAA

FIGURE 109

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53977

<subunit 1 of 1, 243 aa, 1 stop

<MW: 27228, pI: 7.43, NX(S/T): 2

MAKVEQVLSLEPQHELKFRGPFTDVVTTNLKLGNPTRNVCFKVKTTAPRRYCVRPNSGIID
AGASINVSVMQLQPFDDYDPNEKSKHKFMVQSMFAPTDTSMEAVWKEAKPEDLMDSKLRCVFE
LPAENDKPHDVEINKIISTTASKTETPIVSKSLSSSLDDTEVKKVMEECKRLQGEVQRLREE
NKQFKEEDGLRMRKTVQSNPISALAPTGKEEGLSTRLLALVVLFFIVGVIIGKIAL

Important features:

Transmembrane domain:

amino acids 224-239

N-glycosylation site.

amino acids 68-71

N-myristoylation site.

amino acids 59-64, 64-69 and 235-240

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FOSTOT 4878460

FIGURE 110

GTCAGTCTTCTAGATTGTCCTTATCCCACCTTTCAACCANTACTCACATTTTCNAGCGCCCAG
GTCCANGTCTGAGCCTGACTTCCCCTTGGGGACCTAGCCTGGAGTCAGGACAATGGNTCGGG
CTGCAGAGGNTTAGAAGCGAGGGCACCAGCAGTTTTGGGTGGGGAGCAAGGGNNGAGAGAAA
CTCTTCAGCGAATCCTTCTAGTACTAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATA
AAAGACNAACCCAGTTCTGTTTGACTATGTAGCATCTTGAAAAGAAAATTATAATAAGCC
CCAAAATTAAGAATTCTTTTGTCATTTTGTCACATTTGCTCTATGGGGGGAATTATTATTTT
ATCATTTTTATTATTTTGCCATTGGAAGGTTAACTTTAAATGAGC

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105101-28182660

FIGURE 111

TATTGTAAAGGCCATTTTAAACCATTTGGTAGGCCTTGGTACATGATGCTGGATTACCTCCTT
AAATGACACCNTTCCTCGCCTGTTGGTGCTGGCCNTTGGGGAGCTGGAGCCCCAGCATGCTG
GGGAGTGCGGTCAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCCAGGCTGCTTT
CCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGAAGCC
CAAAGGAATTGCCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGTTGA
CTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAAGCT
AAATTGTATTGGTTCATGTAGTGAAGTCAAAGTGTATTTCAGAGATGTTTAATGCATATTTA
ACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAATGCTGCG
TGCTGCTGAACTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTG

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FIGURE 112

CCCTGGTGGTTTTGTTCTTTAATTCGTTGGTGTAATTNTTGGGAAGATTGCTTGTAGAGGTA
GNATGCACCNGGCTGGTAAATTGGATTGGTGGATCCACCATATCCATGGGATTTAAATTTAT
CATAACCATGTGTAAAAAGAAATTAATGTATGATGACATNTCACAGGTATTGCCTTTAAATT
ACCCATCCCTGNANACACATACACAGATACACANANACAAATNTAATGTAACGATNTTTTAG
AAAGTTAAAAATGTATAGTAAC

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FIGURE 113

GGTGGCCCATTCCTGGCCAGGCTGCTTTCGGTNTTCAGTTCTGTCCAAGCCATCAGCTCC
TTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATNAGACGTAC
TTGTNATAAGTGAGAGGCGTGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGT
GCTTTGTTTANTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAAGT
TTATTCAGAGATGTTTAATGCATATTTAANTTATTTAATGTATTTNATNTCATGTTTTCTTA
TTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAANTNTGTTGGGTGAACTGGTATTGC
TGCTGGAGGGCTGTGGGCTCCTCTGTCTTTGGAGAGTCTGGTCATGTGGAGGTGGG

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FIGURE 114

TGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTTGATGAACAGAGTC
AGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTG
TGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGAC
CAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAAGTGTATTTCAGAGATGTTTAATGC
ATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAA
TGCTGCGTGC

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FIGURE 115

AAACCTTTAAAAGTTGAGGGGAAAAGAATGATCCTTTATTAATGACAAGGGAAACCN TGNGT
AATGCCACAATGGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCTTGGTACATGATGC
TGGATTACCTCTCTTAAAATGACACCCTTCCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTN
GAGCCCAGCATGCTGGGGAGTGCGGTCTGCTCCACACAGTAGTCCCCANGTGGCCCANTCCC
GGCCCAGGCTGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGANTGATGA
ACAGAGTCAGAAGCCCAAAGGAATTGCANTGTGGCAGCATCAGANGTANTNGTCATAAGTGA
GAGGCGTGTGTTGANTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTcantt
AAAGGGNCCAAGNTAAATTTGTATTGGTTCATGTAGTGAAGTCAAANTGTTATTCAGAGATG
TTTAATGCATATTTAANTTATTTAATGTATTTcatntcatgTTTTCTTATTGTCACAAGGGT
ACAGTTAATGCTGCGTGCTGCTGAANTCTGTTGGGTGAANTGGTATTGCTG

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FIGURE 116

GGCCCTTGGGGAGCTGGAGCCCAGCATGCTGGGGAGTGCGGTCAGCTCCACACAGTAGTCCC
CACGTGGCCCACTCCCGGCCCAGGCTGCTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGC
TCCTTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACG
TACTCGTCATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGC
AGTGCTTTGTTCACTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAA
CTGTTATTCAGAGATGTTTAATGCATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTTC
TTATTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAACTCTGTTGGGTGAACTGGTAT
TGCTGCTGGAGGGCTGTGGGCTCCTCTGTCTCTGGAGAGTCTGGTCATGTGGAGGTGGG

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FIGURE 117

CGAGCTCCGGGTGCTGTGGCCCCGGCCTTGGCGGGGGCGGCCTCCGGCTCAGGCTGGCTGAGA
GGCTCCCAGCTGCAGCGTCCCCGCCCCGCTCCTCGGGAGCTCTGATCTCAGCTGACAGTGCC
CTCGGGGACCAAACAAGCCTGGCAGGGTCTCACTTTGTTGCCAGGCTGGAGTTCAGTGCCA
TGATCATGGTTTACTGCAGCCTTGACCTCCTGGGTTCAAGCGATCCTGCTGAGTAGCTGGGA
CTACAGGACAAAATTAGAAGATCAAAATGGAAAATATGCTGCTTTGGTTGATATTTTTTCACC
CCTGGGTGGACCCTCATTGATGGATCTGAAATGGAATGGGATTTTATGTGGCACTTGAGAAA
GGTACCCCGGATTGTGTCAGTGAAAGGACTTTCCATCTCACCAGCCCCGCATTTGAGGCAGATG
CTAAGATGATGGTAAATACAGTGTGTGGCATCGAATGCCAGAAAGAACTCCCAACTCCCAGC
CTTTCTGAATTGGAGGATTATCTTTTCTATGAGACTGTCTTTGAGAATGGCACCCGAACCTT
AACCAGGGTGAAAGTTCAAGATTTGGTTCTTGAGCCGACTCAAAATATCACCACAAAGGGAG
TATCTGTTAGGAGAAAGAGACAGGTGTATGGCACCGACAGCAGGTTGAGCATCTTGACAAA
AGGTTCTTAACCAATTTCCCTTTTCTAGCACAGCTGTGAAGCTTTCCACGGGCTGTAGTGGCAT
TCTCATTTCCTTCAGCATGTTCTAACTGCTGCCACTGTGTTTATGATGGAAAGGACTATG
TCAAAGGGAGTAAAAAGCTAAGGGTAGGGTTGTTGAAGATGAGGAATAAAAGTGGAGGCAAG
AAACGTCGAGGTTCTAAGAGGAGCAGGAGAGAAGCTAGTGGTGGTGACCAAAGAGAGGGTAC
CAGAGAGCATCTGCAGGAGAGAGCGAAGGGTGGGAGAAGAAGAAAAAATCTGGCCGGGGTC
AGAGGATTGCCGAAGGGAGGCCTTCTTTTCTAGTGGACCCGGGTCAAGAATACCCACATTCCG
AAGGGCTGGGCACGAGGAGGCATGGGGGACGCTACCTTGGAATATGACTATGCTCTTCTGGA
GCTGAAGCGTGCTCACAAAAGAAATACATGGAACCTTGAATCAGCCCAACGATCAAGAAAA
TGCCTGGTGAATGATCCACTTCTCAGGATTTGATAACGATAGGGCTGATCAGTTGGTCTAT
CGGTTTTGTCAGTGTGTCCGACGAATCCAATGATCTCCTTTACCAATACTGCGATGCTGAGTC
GGGCTCCACCGGTTTCGGGGGTCTATCTGCGTCTGAAAGATCCAGACAAAAGAATTGGAAGC
GCAAAATCATTGCGGTCTACTCAGGGCACCAGTGGGTGGATGTCCACGGGGTTTCAAGAGGAC
TACAACGTTGCTGTTTCGCATCACTCCCTTAAATACGCCCAGATTTGCCTCTGGATTACGG
GAACGATGCCAATTGTGCTTACGGCTAACAGAGACCTGAAACAGGGCGGTGTATCATCTAAA
TCACAGAGAAAACCAGCTCTGCTTACCGTAGTGAGATCACTTCATAGGTTATGCCTGGACTT
GAACTCTGTCAATAGCATTTCACATTTTTTCAAAATCAGGAGATTTTCGTCCATTTAAAAAA
TGTATAGGTGCAGATATTGAAACTAGGTGGGCACTTCAATGCCAAGTATATACTCTTCTTTA
CATGGTGATGAGTTTCATTTGTAGAAAAATTTTGTGCTTCTTAAAAATTAGACACACTTT
AAACCTTCAAACAGGTATTATAAATAACATGTGACTCCTTAATGGACTTATTCTCAGGGTCC
TACTCTAAGAAGAATCTAATAGGATGCTGGTTGTGTATTAAATGTGAAATTGCATAGATAAA
GGTAGATGGTAAAGCAATTAGTATCAGAATAGAGACAGAAAGTTACAACACAGTTTGTACTA
CTCTGAGATGGATCCATTGAGCTCATGCCCTCAATGTTTATATTGTGTTATCTGTTGGGTCT
GGGACATTTAGTTTGTGTTTTTTTGAAGAATTACAAATCAGAAGAAAAAGCAAGCATTATAAA
CAAACTAATAACTGTTTTTACTGCTTTAAGAAATAACAATTACAATGTGTATTATTTAAAAA
TGGGAGAAATAGTTTGTCTATGAAATAAACCTAGTTTAGAAATAGGGAAGCTGAGACATTT
TAAGATCTCAAGTTTTTATTTAATACTCAAAATATGGACTTTTCATGTATGCATAGGG
AAGACACTTCACAAATTATGAATGATCATGTGTGAAAGCCACATTATTTTATGCTATACAT
TCTATGTATGAGGTGCTACATTTTTTAGGACAAAGAATTCTGTAATCTTTTTCAAGAAAGAGT
CTTTTTCTCCTTGACAAAATCCAGCTTTTGTATGAGGACTATAGGGTGAATTCTCTGATTAG
TAATTTTAGATATGTCCTTTCTTAAAAATGAATAAAATTTATGAATATGA

FIGURE 118

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253

<subunit 1 of 1, 413 aa, 1 stop

<MW: 47070, pI: 9.92, NX(S/T): 3

MENMLLWLIFFTPGWTLIDGSEMEWDFMWHLRKVPRIVSERTFHLTSPAFAEADAKMMVNTVC
GIECQKELPTPSLSELEDYLSYETVFENGTRTLTRVKVQDLVLEPTQNITTKGVSVRRKRQV
YGTDSRFSILDKRFLTNFPFSTAVKLSTGCSGILISPQHVLTAAHCVHDGKDYVKGSKKLRV
GLLKMRNKSGGKKRRGSKRSRREASGGDQREGTREHLQERAKGRRRKSGRGQRIAEGRPS
FQWTRVKNTHIPKGWARGGMGDATLDYDYALLELKRAHKKKYMELGISPTIKKMPGGMIHFS
GFDNDRADQLVYRFCVSVDESNDLLYQYCDAESGSTGSGVYLRLKDPDKKNWKRKIIAVYSG
HQWVDVHGVQKDYNVAVRITPLKYAQICLWIHGNDANCAYG

Important features:

Signal peptide:

amino acids 1-16

N-glycosylation sites.

amino acids 90-93, 110-113 and 193-196

Glycosaminoglycan attachment site.

amino acids 236-239

Serine proteases, trypsin family, histidine active site.

amino acids 165-170

09978187-101501

FIGURE 119

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTTAGCACCAGTACTGGAT
GTGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTCAGTGTCCGATTCTGATTCCGGCAAGG
ATCCAAGCATGGAATGCTGCCGTGCGGCAACTCCTGGCACACTGCTCCTCTTTCTGGCTTTC
CTGCTCCTGAGTTCCAGGACCGCACGCTCCGAGGAGGACCGGGACGGCCTATGGGATGCCTG
GGGCCCATGGAGTGAATGCTCACGCACCTGCGGGGGAGGGGCCTCCTACTCTCTGAGGCGCT
GCCTGAGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGAC
TGCCCACCAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCA
CCATGGCCAGTTTTATGAATGGCTTCCTGTGTCTAATGACCCTGACAACCCATGTTCACTCA
AGTGCCAAGCCAAAGGAACAACCCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTACG
CGTTGCTATACAGAATCTTTGGATATGTGCATCAGTGGTTTATGCCAAATTGTTGGCTGCGA
TCACCAGCTGGGAAGCACCGTCAAGGAAGATAACTGTGGGGTCTGCAACGGAGATGGGTCCA
CCTGCCGGCTGGTCCGAGGGCAGTATAAATCCCAGCTCTCCGCAACCAAATCGGATGATACT
GTGGTTGCACTTCCCTATGGAAGTAGACATATTCGCCTTGTCTTAAAAGGTCCTGATCACTT
ATATCTGGAAACCAAACCCCTCCAGGGGACTAAAGGTGAAAACAGTCTCAGCTCCACAGGAA
CTTTCCTTGTGGACAATTCTAGTGTGGACTTCCAGAAATTTCCAGACAAAGAGATACTGAGA
ATGGCTGGACCACTCACAGCAGATTTCAATTGTCAAGATTCGTAACCTCGGGCTCCGCTGACAG
TACAGTCCAGTTCATCTTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCTTTC
CTTGCTCAGCAACCTGTGGAGGAGGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGG
AGCAACCGTGTGGTTGCTGACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACC
CAAGCTTCAGGAGTGCAACTTGGATCCTTGTCCAGCCAGTGACGGATACAAGCAGATCATGC
CTTATGACCTCTACCATCCCCTTCCTCGGTGGGAGGCCACCCCATGGACCGCGTGCTCCTCC
TCGTGTGGGGGGGGCATCCAGAGCCGGGCAGTTTCCTGTGTGGAGGAGGACATCCAGGGGCA
TGTCACTTTCAGTGGAAGAGTGGAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCT
GCAACATTTTTGACTGCCCTAAATGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGT
GGCCAGGGCCTCAGATACCGTGTGGTCCTCTGCATCGACCATCGAGGAATGCACACAGGAGG
CTGTAGCCCCAAAAACAAAGCCCCACATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATA
AACCCAAAGAGAAACTTCCAGTCGAGGCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTA
GAAGAAGGAGCTGCTGTGTCAGAGGAGCCCTCGTAAGTTGTAAAAGCACAGACTGTTCTATA
TTTGAAACTGTTTTGTTTAAAGAAAGCAGTGTCTCACTGGTTGTAGCTTTCATGGGTTCTGA
ACTAAGTGTAATCATCTCACCAAAGCTTTTTGGCTCTCAAATTAAAGATTGATTAGTTTCAA
AAAAAAAAA

FIGURE 120

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847

<subunit 1 of 1, 525 aa, 1 stop

<MW: 58416, pI: 6.62, NX(S/T): 1

MECCRRATPGTLLLFLAFLLLSSRTARSEEDRDGLWDAWGPWSECSRTC GGGASYS LRRLCLS
SKSCEGRNIRYRTC SNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNDPDNPCSLKCQ
AKGTTLVVELAPKVLDGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCR
LVRGQYKSQLSATKSDDTVVALPYGSRHIRLV LKGPDHLYLETKTLQGTKGENSL SSTGTFL
VDNSSVDFQKFPDKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFFP CS
ATCGGGYQLTSAECYDLRSNRVVADQYCHYPENIKPKPKLQECNLDPCPASDGYKQIMPYD
LYHPLPRWEATPWTACSSSCGGGIQSRAVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNI
FDCPKWLAQEWSPCTVTCGQGLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPK
EKLPVEAKLPWFKQAQELEEAAVSEEPS

Important features:

Signal peptide:

amino acids 1-25

N-glycosylation site.

amino acids 251-254

Thrombospondin 1

amino acids 385-399

von Willebrand factor type C domain proteins

amino acids 385-399, 445-459 and 42-56

09978187 287660

FIGURE 121

CGGACGCGTGGGCGGCGGCTGCGGAACTCCCGTGGAGGGGCCGGTGGGCCCTCGGGCCTGAC
AGATGGCAGTGGCCACTGCGGCGGCAGTACTGGCCGCTCTGGGCGGGGCGCTGTGGCTGGCG
GCCCCCGGTTTCGTGGGGCCCAGGGTCCAGCGGCTGCGCAGAGGCGGGGACCCCGGCCTCAT
GCACGGGAAGACTGTGCTGATCACCGGGGCGAACAGCGGCCTGGGCCGCGCCACGGCCGCCG
AGCTACTGCGCCTGGGAGCGCGGGTGATCATGGGCTGCCGGGACCGCGCGCGCGCCGAGGAG
GCGGCGGGTCAGCTCCGCCGCGAGCTCCGCCAGGCCGCGGAGTGCGGCCCAGAGCCTGGCGT
CAGCGGGGTGGGCGAGCTCATAGTCCGGGAGCTGGACCTCGCCTCGCTGCGCTCGGTGCGCG
CCTTCTGCCAGGAAATGCTCCAGGAAGAGCCTAGGCTGGATGTCTTGATCAATAACGCAGGG
ATCTTCCAGTGCCCTTACATGAAGACTGAAGATGGGTTTGAGATGCAGTTCGGAGTGAACCA
TCTGGGGCACTTTCTACTACCAATCTTCTCCTTGGA CTCTCAAAGTTTCAGCTCCCAGCA
GGATTGTGGTAGTTTCTTCCAACTTTATAAATACGGAGACATCAATTTTGATGACTTGAAC
AGTGAACAAAGCTATAATAAAAGCTTTTGTTATAGCCGGAGCAAAGTGGCTAACATTCTTTT
TACCAGGGAAGTAGCCCGCCGCTTAGAAGGCACAAATGTCACCGTCAATGTGTTGCATCCTG
GTATTGTACGGACAAATCTGGGGAGGCACATACACATTCCACTGTTGGTCAAACCACTCTTC
AATTTGGTGT CATGGGCTTTTTTCAAAGTCCAGTAGAAGGTGCCAGACTTCCATTTATTT
GGCCTCTTCACCTGAGGTAGAAGGAGTGTCAGGAAGATACTTTGGGGATTGTAAAGAGGAAG
AACTGTTGCCCAAAGCTATGGATGAATCTGTTGCAAGAAAGTCTGGGATATCAGTGAAAGTG
ATGGTTGGCCTGCTAAAATAGGAACAAGGAGTAAAAGAGCTGTTTATAAAAGTGCATATCAG
TTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTTACTTGAAGAAAAAGAATTTTG
ATATTGGAATAGCCTGCTAAGAGGTACATGTGGGTATTTTGGAGTTACTGAAAAATTATTTT
TGGGATAAGAGAATTTTCAGCAAAGATGTTTTAAATATATATAGTAAGTATAATGAATAATAA
GTACAATGAAAAATACAATTATATTGTAAAATTATAACTGGGCAAGCATGGATGACATATTA
ATATTTGTCAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTTTTCAAGTATCTTTGAGTT
TCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTGTTGTGTGGAAATTATCTGC
CTGGTGTGTGCACACAAGTCTTACTTGGAATAAATTTACTGGTAC

FIGURE 122

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58747

<subunit 1 of 1, 336 aa, 1 stop

<MW: 36865, pI: 9.15, NX(S/T): 2

MAVATAAAVLAAALGGALWLAARRFVGPRVQRLRRGGDPGLMHGKTVLITGANSGLGRATAAE
LLRLGARVIMGCRDRARAEEAAGQLRRELQRQAECGPEPGVSGVGELIVRELDLASLRSVRA
FCQEMLQEEPRLDVLINNAGIFQCPYMKTEDGFEMQFGVNHLLGHFLLTNLLLGLLKSSAPSR
IVVVSSKLYKYGDINFDDLNSEQSYNKSFCYSRSLANILFTRELARRLEGNTNVTNVNLHPG
IVRTNLGRHIHIPLLVKPLFNLVSWAFFKTPVEGAQTSIYLASSPEVEGVSGRYFGDCKEEE
LLPKAMDESVARKLWDISEVMVGLLK

Important features:

Signal peptide:

amino acids 1-21

Short-chain alcohol dehydrogenase family protein

amino acids 134-144, 44-56 and 239-248

N-glycosylation site.

amino acids 212-215 and 239-242

FIGURE 123

GGGGATTGTAAAGAGGAAGNACTGTGCCCAAAGNTATGGATGAATCTGTTGCAAGAAAATTN
TGGGATATCAGTGAAGTGATGGTTNGCCTGCTAAAATAGGAACAAGGAGTAAAAGAGCTGTT
TATAAACTGCATATCAGTTATATCTGTGATCAGGAATGGTGTGGATTGAGAAGTTGTTACT
TGAAGAAAAAGAATTTTGATATTGGAATAGCCTGNTAAGAGGNACATGTGGGTATTTTGGAG
TTACTGAAAAATTATTTTTGGGATAAGAGAATTTTCAGCAAAGATGTTTTAAATATATATAGT
AAGTATAATGAATAATAAGTACAATGAAAAATACAATTATATTGTAAAATTATAACTGGGCA
AGCATGGATGACATATTAATATTTGTGAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTT
TTCAAGTATCTTTGAGTTTCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTT
TGTGTGGAAATTATCTGCCTGGCTT

105101 2878660

FIGURE 124

GAGAGGACGAGGTGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCGGCTCCCGGAGCCCAGCC
CTTTCCTAACCCAACCCAACCTAGCCCAGTCCCAGCCGCCAGCGCCTGTCCCTGTCACGGAC
CCCAGCGTTACCAATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCT
GCTCCTGGTAACTTGGGTTTTTACTCCTGTAACAACTGAAATAACAAGTCTTGCTACAGAGA
ATATAGATGAAATTTTAAACAATGCTGATGTTGCTTTAGTAAATTTTTATGCTGACTGGTGT
CGTTTCAGTCAGATGTTGCATCCAATTTTTGAGGAAGCTTCCGATGTCATTAAGGAAGAATT
TCCAAATGAAATCAAGTAGTGTGGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCC
AGAGATACAGGATAAGCAAATACCCAACCCTCAAATTGTTTCGTAATGGGATGATGATGAAG
AGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGCAACAAAAAAG
TGACCCCATTTCAAGAAATTCGGGACTTAGCAGAAATCACCCTCTTGATCGCAGCAAAAGAA
ATATCATTGGATATTTTGAGCAAAAGGACTCGGACAACCTATAGAGTTTTTGAACGAGTAGCG
AATATTTTGCATGATGACTGTGCCTTTCTTTCTGCATTTGGGGATGTTTCAAACCGGAAAG
ATATAGTGGCGACAACATAATCTACAAACCACCAGGGCATTCTGCTCCGGATATGGTGTACT
TGGGAGCTATGACAAATTTTGATGTGACTTACAATTGGATTCAAGATAAATGTGTTCTCTT
GTCCGAGAAATAACATTTGAAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTTTCTCAT
ACTCTTTCACATGAAAGAAGATACAGAAAGTTTAGAAATATTCAGAATGAAGTAGCTCGGC
AATTAATAAGTGAAAAAGGTACAATAAACTTTTTACATGCCGATTGTGACAAATTTAGACAT
CCTCTTCTGCACATACAGAAAACCTCCAGCAGATTGTCTGTAAATCGCTATTGACAGCTTTAG
GCATATGTATGTGTTTGGAGACTTCAAAGATGTATTAATTCCTGGAAAACCTCAAGCAATTCTG
TATTTGACTTACATTCTGGAAAACCTGCACAGAGAATTCCATCATGGACCTGACCCAACTGAT
ACAGCCCCAGGAGAGCAAGCCCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTTCCAGAA
ACTAGCACCCAGTGAATATAGGTATACTCTATTGAGGGATCGAGATGAGCTTTTAAAAACTTG
AAAAACAGTTTGTAAGCCTTTCAACAGCAGCATCAACCTACGTGGTGGAAATAGTAAACCTA
TATTTTCATAATTCTATGTGTATTTTTATTTTGAATAAACAGAAAGAAATTTAAAAA
AAAAA

FIGURE 125

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57689

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46927, pI: 5.21, NX(S/T): 0

MHPAVFLSLPDLRCSLLLLVTWVFTPVTTEITSLATENIDEILNNADVALVNFYADWCRFSQ
MLHPIFEEASDVIKEEFPNENQVV FARVDCDQHSDIAQRYRISKYPTLKLFRNGMMMKREYR
GQRSVKALADYIRQQKSDPIQEIRDLAEITTLDRSKRNIIGYFEQKDSDN YRVFERVANILH
DDCAFLSAFGDVSKPERYSGDNIIYKPPGHSAPDMVYLGAMTNFDVTYNW IQDKCVPLVREI
TFENGEEELTEEGLPFLILFHMKEDTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLH
IQKTPADCPVIAIDSFRHMYVFGDFKDVLI PGKLKQFVFDLHSGKLHREFHHGPDPTDTAPG
EQAQDVASSPPESSFQKLAPSEYRYTLLRDRDEL

Important features:

Signal peptide:

amino acids 1-29

Endoplasmic reticulum targeting sequence.

amino acids 403-406

Tyrosine kinase phosphorylation site.

amino acids 203-211

Thioredoxin family proteins

amino acids 50-66

09978187-101501

FIGURE 126

ATTAAGGAAGAATTTCCAAATGAAAATCAAGTAGTNTTTGCCAGAGTNGATTGTGATCAGCA
CTCTGACATAGCCCAGAGATACAGGATAAGCAAATACCCAACCCTCAAATTGTTTCGTAATG
GGATGATGATGAAGAGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTA

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TOSTOT-282660

FIGURE 127

AGAGGCCTCTCTGGAAGTTGTCCCGGGTGTTCGCCGCNNGAGCCCGGGTCGAGAGGACNAGG
TGCCGCTGCCTGGAGAATCCTCCGCTGCCGTGGCTCCCGGAGCCCAGCCCTTTCCTAACCC
AACCCAACCTAGCCCNGTCCCAGCCGCCAGCGCCTGTCCCTGTCNCGGANCCCAGCGTNACC
ATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCTGCTCCTGGTAAC
TTGGGTTTTTACTCCTGTAACAACCTGAAATAACNNGTCTTGATACNNAGAATATAGATGAAA
TTTTAAACNATGCTGATGTGGCTTTAGTCAATTTTTATGCTGACTGGTGTGTTTTAGTCAG
ATGTGGCATCCAATTTTTGAGGANGCTTCCGATGTCATTAAGGAAGAATTTCCAAATGAAAA
TCAAGTAGTGTTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCCAGAGATACAGGA
TAAGCAAATACCCAACCCTCAAATTGTTTCGTAATGGGATGATGATGAAGAGAGAATACAGG
GGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGC

09978187-101501
TOTOT-878760

FIGURE 128

GCCCACGCGTCCGATGGCGTTACGTTTCGCGGCCTTCTGCTACATGCTGGCGCTGCTGCTCA
CTGCCGCGCTCATCTTCTTCGCCATTTGGCACATTATAGCATTTGATGAGCTGAAGACTGAT
TACAAGAATCCTATAGACCAGTGTAATACCCTGAATCCCCTTGACTCCCAGAGTACCTCAT
CCACGCTTTCTTCTGTGTCATGTTTCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATA
TGCCCCTCTTGGCATATCATATTTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCCAGGA
CTCTATGACCCTACAACCATCATGAATGCAGATATTCTAGCATATTGTCAGAAGGAAGGATG
GTGCAAATTAGCTTTTTTATCTTCTAGCATTTTTTTTACTACCTATATGGCATGATCTATGTTT
TGGTGAGCTCTTAGAACAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAAGCCAC
CAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGT
TACTTTAAAAAATGACTCCTTATTTTTTAAATGTTTCCACATTTTTTGCTTGTGGAAGACTG
TTTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAATTAATATAAAAT
GATTACCTCTGGTGTTGACAGGTTTGAACCTTGCACTTCTTAAGGAACAGCCATAATCCTCTG
AATGATGCATTAATTACTGACTGTCCTAGTACATTGGAAGCTTTTGTTTATAGGAACCTTGTA
GGGCTCATTTTGGTTTCATTGAAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGTGC
TTCTGATGAAGTGAAAATGTATATCTGACTAGTGGGAACTTCATGGGTTTCCTCATCTGTC
ATGTCGATGATTATATATGGATACATTTACAAAAATAAAAAGCGGGAATTTTCCCTTCGCTT
GAATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGAGTAATAAA
TATACTTGCTTTAATTCTTAAGCATAAGTAAACATGATATAAAAAATATATGCTGAATTACTT
GTGAAGAATGCATTTAAAGCTATTTTAAATGTGTTTTTATTTGTAAGACATTACTTATTAAG
AAATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAGAATTTGCAGG
TACTACAGATTTTCAAACTGAATGAGAGAAAATTGTATAACCATCCTGCTGTTCTTTAGT
GCAATACAATAAACTCTGAAATTAAGACTC

FIGURE 129

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23330

<subunit 1 of 1, 144 aa, 1 stop

<MW: 16699, pI: 5.60, NX(S/T): 0

MAFTFAAFCYMLALLLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFF
CVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKLA
FYLLAFFYYLYGMIYVLVSS

Important features:

Signal peptide:

amino acids 1-20

Type II transmembrane domain:

amino acids 11-31

Other transmembrane domain:

amino acids 57-77 and 123-143

09978187-101501

FIGURE 130

ATTATAGCATTTGATGAGCTGAAGACTGATTACAAGATCCTATAGACCAGTGTAATACCCTG
AATCCCCTTGTA TACTCCCAGAGTACCTCATCCACGCTTTCTTCTGTGTCATGTTTCTTTGTGC
AGCAGAGTGGCTTACACTGGGTCTCAATATGCCCTCTTGGCATATCATATTTGGAGGTATA
TGAGTAGACCAGTGATGAGTGGCCCAGGACTCTATGACCCTACAACCATCATGAATGCAGAT
ATTCTAGCATATTGTCAGAAGGAAGGATGGTGCAAATTAGCTTTTTATCTTCTAGCATTTTT
TTACTACCTATATGGCATGATCTATGTTTTGGTGAGCTCTTAGAACAACACACAGAAGAATT
GGTCCAGTTAAGTGCATGCAAAAAGCCACCAAATGAAGGGATTCTATCCAGCAAGATCCTGT
CCAAGAGTAGCCTGTGGAATCTGATCAGTTACTTTAAAAAATG

09978187.101501

FIGURE 131

CGGACGCGTGGGGGAAACCCCTTCCGAGAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGG
GAACAAGATGGCGGCGCCGAAGGGGAGCCTCTGGGTGAGGACCCAACTGGGGCTCCCGCCGC
TGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTGCGGGACCGCTTCGGCTGAAGCATTTGAC
TCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGACAC
CTACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTC
AGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACA
GAAGCATATTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCC
ATTCGCTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTC
CTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACC
TCTTCATGGACTTTTTATCTTCAAGCCGATGACGGAAAAATAGTTATATTCCAGTCTAAGCC
AGAAATCCAGTACGCACCACATTTGGAGCAGGAGCCTACAAATTTGAGAGAATCATCTCTAA
GCAAAATGTCCTATCTGCAAATGAGAAATTCACAAGCGCACAGGAATTTTCTTGAAGATGGA
GAAAGTGATGGCTTTTTAAGATGCCTCTCTCTTAACTCTGGGTGGATTTTAACTACAACCTCT
TGTCTCTCGGTGATGGTATTGCTTTGGATTTGTTGTGCAACTGTTGCTACAGCTGTGGAGC
AGTATGTTCCCTCTGAGAAGCTGAGTATCTATGGTGACTTGGAGTTTATGAATGAACAAAAG
CTAAACAGATATCCAGCTTCTTCTCTTGTGGTTGTTAGATCTAAAACTGAAGATCATGAAGA
AGCAGGGCCTCTACCTACAAAAGTGAATCTTGCTCATTCTGAAATTTAAGCATTTTTCTTTT
AAAAGACAAGTGTAATAGACATCTAAAATTCCACTCCTCATAGAGCTTTTAAATGGTTTCA
TTGGATATAGGCCTTAAGAAATCACTATAAAATGCAAATAAAGTTACTCAAATCTGTG

FIGURE 132

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA26847

<subunit 1 of 1, 323 aa, 1 stop

<MW: 36223, pI: 5.06, NX(S/T): 1

MAAPKGS LWVRTQLGLPPLLLLT MALAGGSGTASAEAFDSVLGDTASCHRA CQLTYPLHTYP
KEEELYACQRG CRLFSICQFVDDGIDLNR TKLECESACTEAYSQSDEQYACHLGCQNQLPFA
ELRQEQLMSLMPKMHLLFPLTLVRSFWSDMMDSAQSFITSSWTFY LQADDGKIVIFQSKPEI
QYAPHLEQEPTNLRESSLSKMSY LQMRNSQAHRNFLEDGESDGF LRCLSLNSGWILTTTLVL
SVMVLLWICCATVATAVEQYVPSEKLSIYGDLEFMNEQKLN RYPASSLVVVRSKTEDHEEAG
PLPTKVNLAHSEI

Important features:

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 241-260

N-glycosylation site.

amino acids 90-93

09978187-101501

FIGURE 133

TTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGCACACCTACCC
TAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTCAGTTTG
TGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACAGAAGCA
TATTCCTCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCCATTCGC
TGAAGTGAAGACAAGAACAACCTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTCCTCTAA
CTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGC

09978187 . 101501

FIGURE 134

CACACTGGCCGGATCTTTTAGAGTCCTTTGACCTTGACCAAGGGTCNGGAAAACAGCAACAA
GCTGAGCTGCTGTGACAGAGGGAACAAGATGGCGGCGCCGAAGGGAGCCTTTGGGTGAGGAC
CCAAGTGGGGCTCCCGCCGCTGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTGCGGGACCG
CTTCGGCTGAAGCATTGACTCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAG
TTGACCTACCCCTTGACACCTACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTG
CAGGCTGTTTTCAATTTGTCAGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGG
AATGTGAATCTGCATGTACAGAAGCATATTCCCAATCTGATGAGCAATATGCTTGCCATCTT
GGTTGCCAGAATCAGCTGCCATTCGCTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCC
AAAAATGCACCTACTCTTTCCTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACT
CCGC

09978187.101501
TOSTOT"28T82660

FIGURE 135

GCGAGGTGGCGATCGCTGAGAGGCAGGAGGGCCGAGGCGGGCCTGGGAGGCGGCCCGGAGGT
GGGGCGCCGCTGGGGCCGGCCCGCACGGGCTTCATCTGAGGGCGCACGGCCCGCGACCGAGC
GTGCGGACTGGCCTCCCAAGCGTGGGGCGACAAGCTGCCGGAGCTGCAATGGGCCGCGGCTG
GGGATTCTTGTTTGGCCTCCTGGGCGCCGTGTGGCTGCTCAGCTCGGGCCACGGAGAGGAGC
AGCCCCCGGAGACAGCGGCACAGAGGTGCTTCTGCCAGGTTAGTGTTACTTGATGATTGT
ACCTGTGATGTTGAAACCATTGATAGATTTAATAACTACAGGCTTTTCCCAAGACTACAAAA
ACTTCTTGAAAGTGACTACTTTAGGTATTACAAGGTAAACCTGAAGAGGCCGTGTCCTTTCT
GGAATGACATCAGCCAGTGTGGAAGAAGGGACTGTGCTGTCAAACCATGTCAATCTGATGAA
GTTCTCTGATGGAATTAAATCTGCGAGCTACAAGTATTCTGAAGAAGCCAATAATCTCATTGA
AGAATGTGAACAAGCTGAACGACTTGGAGCAGTGGATGAATCTCTGAGTGAGGAAACACAGA
AGGCTGTTCTTCAGTGGACCAAGCATGATGATTCTTCAGATAACTTCTGTGAAGCTGATGAC
ATTCAGTCCCCTGAAGCTGAATATGTAGATTTGCTTCTTAATCCTGAGCGCTACACTGGTTA
CAAGGGACCAGATGCTTGGAATAATGGAATGTCATCTACGAAGAAAACGTGTTTTAAGCCAC
AGACAATTAAAAGACCTTTAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGAACACT
TTTTACAGTTGGCTAGAAGGTCTCTGTGTAGAAAAAGAGCATTCTACAGACTTATATCTGG
CCTACATGCAAGCATTAAATGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAG
AAAAGAAATGGGGACACAACATTACAGAATTTCAACAGCGATTTGATGGAATTTTGACTGAA
GGAGAAGGTCCAAGAAGGCTTAAGAACTTGTATTTTCTCTACTTAATAGAACTAAGGGCTTT
ATCCAAAGTGTTACCATTCTTCGAGCGCCAGATTTTCAACTCTTTACTGGAAATAAAATTC
AGGATGAGGAAAACAAAATGTTACTTCTGGAAATACTTCATGAAATCAAGTCATTTCTTTG
CATTTTGATGAGAATTCATTTTTTGTCTGGGGATAAAAAAGAAGCACACAACTAAAGGAGGA
CTTTCGACTGCATTTTAGAAATATTTCAAGAATTATGGATTGTGTTGGTTGTTTTAAATGTC
GTCTGTGGGGAAAGCTTCAGACTCAGGGTTTGGGCACTGCTCTGAAGATCTTATTTTCTGAG
AAATTGATAGCAAATATGCCAGAAAGTGGACCTAGTTATGAATTCCATCTAACCAGACAAGA
AATAGTATCATTATTCAACGCATTTGGAAGAATTTCTACAAGTGTGAAAGAATTAGAAAAC
TCAGGAACTTGTTACAGAATATTCATTAAAGAAAACAAGCTGATATGTGCCTGTTTCTGGAC
AATGGAGGCGAAAGAGTGGAATTTCAATCAAAGGCATAATAGCAATGACAGTCTTAAGCCAA
ACATTTTATATAAAGTTGCTTTTGTAAAGGAGAATTATATTGTTTTAAGTAAACACATTTT
AAAAATTGTGTTAAGTCTATGTATAATACTACTGTGAGTAAAAGTAATACTTTAATAATGTG
GTACAAATTTTAAAGTTTAATATTGAATAAAAGGAGGATTATCAAATTAATAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 136

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53974

<subunit 1 of 1, 468 aa, 1 stop

<MW: 54393, pI: 5.63, NX(S/T): 2

MGRGWGFLFGLLGAVWLLSSGHGEEQPPETAAQRCFCQVSGYLDDCTCDVETIDRFNNYRLF
PRLQKLLESDYFRYYKVNLRPCPFWNDISQCGRDCAVKPCQSDEVDPGDKSASYKYSEEA
NNLIEECEQAERLGAVDESLSEETQKAVLQWTKHDDSSDNFCEADDIQSPEAEYVDLLLNPE
RYTGYKGPDAWKIWNVIYEENCFKPQTIKRPLNPLASGQGTSEENTFYSWLEGLCVEKRAFY
RLISGLHASINVHLSARYLLQETWLEKKWGHNITEFQQRFDGILTEGEGPRRLKNLYFLYLI
ELRALSQVLPFFERPDLFTGNKIQDEENKMLLLEILHEIKSFPLHFDENSFFAGDKKEAH
KLKEDFRLHFRNISRIMDCVGCFCRLWGKLQTQGLGTALKILFSEKLIANMPESGPSYEFH
LTRQEIVSLFNAFGRISTSVKELENFRNLLQNIH

Important features:

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 280-283 and 384-387

Amidation site.

amino acids 94-97

Glycosaminoglycan attachment site.

amino acids 20-23 and 223-226

Aminotransferases class-V pyridoxal-phosphate

amino acids 216-222

Interleukin-7 proteins

amino acids 338-343

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FIGURE 137

GCTGGAAATATGGATGTCATCTACGAGAACTGTTTTAAGCCACAGACAATTAAAAGACCTT
TAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGNACACTTTTTACAGTTGGCTAGAA
GGTCTCTGTGTAGAAAAAAGAGCATTCTACAGACTTATATCTGGCCTACATGCAAGCATTAA
TGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAGAAAAGAAATGGGGACACA
ACATTACAGAATTTNAACAGCGATTTGATGGAATTTTGACTGAAGGAGAAGGTCCAAGAAGG
CTTAAGAACTTGTATTTTCTCTACTTAATAGAACTAAGGGCTTTATCCAAAGTGTTACCATT
CTTNGAGCGCCCAGATTTTCAACTNNTTTACTGGAAATAAAATTCAGGATGAGGNAAACAAAA
TGTTACTTTTGGAAATACTTCATGAAATCAAGTCATTTCTTTGCATTTTGATGAGAATTCA
TTTTTTTGCTG

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TOS FOR "LBIS/650

FIGURE 138

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTTGGGAGGGGGCAGGATGGGAGGGAA
AGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGACTTCTCATACTGGACAGAAAC
CGATCAGGCATGGAACTCCCCTTCGTCACTCACCTGTTCTTGCCCCCTGGTGTTCCTGACAGG
TCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCTATTCCCAGGGCCACCAGAAG
CTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGACAGCGATGGATGCTGGTGGGC
GCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTTTATCGCTGCCCTGTAGGGGG
GGCCCACAATGCCCCATGTGCCAAGGGGCCACTTAGGTGACTACCAACTGGGAAATTCATCTC
ATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGACAGATGGTGTATGGGGGATTC
ATGGTGAGCTAAGGAGAGGGTGGTGGCAGTGTCTCTGAAGGTCCATAAAAGAAAAAGAGAA
GTGTGGTAAGGGAAAATGGTCTGTGTGGAGGGGTCAAGGAGTTAAAAACCCTAGAAAGCAAA
AGGTAGGTAATGTCAGGGAGTAGTCTTCATGCCTCCTTCAACTGGGAGCATGTTCTGAGGGT
GCCCTCCCAAGCCTGGGAGTAACTATTTCCCCCATCCCCAGGCCTGTGCCCCCTCTCTGGTCT
CGTGCTTGTGGCAGCTCTGTCTTCAGTTCTGGGATATGTGCCCGTGTGGATGCTTCATTCCA
GCCTCAGGGAAGCCTGGCACCCACTGCCCAACGTGAGCCAGAGGAAGGCTGAGTACTTGGTT
CCCAGAAGGAGATACTGGGTGGGAAAAAGATGGGGCAAAGCGGTATGATGCCTGGCAAAGGG
CCTGCATGGCTATCCTCATTGCTACCTAATGTGCTTGCAAAAGCTCCATGTTTCCTAACAGA
TTCAGACTCCTGGCCAGGTGTGGTGGCCACACCTGTAATTCTAGCACTTTGGGAGGCCAAG
GTGGGCAGATCACTTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACTCCAT
CTCTACTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA
ATCTACTCGGGAGGCTAAGACAGGAGACTCTCACTTCAACCCAGGAGGTGGAGGTTGCGGTG
AGCCAAGATTGTGCCTCTGCACTCTAGCGTGGGTGACAGAGTAAGCGAGACTCCATCTCAAA
AATAATAATAATAATAATTCAGACTCCTTATCAGGAGTCCATGATCTGGCCTGGCACAGTAA
CTCATGCCTGTAATCCCAACATTTTGGGAGGCCAACGCAGGAGGATTGCTTGAGGTCTGGAG
GTTTGAGACCAGCCTGGGCAACATAGAAAGACCCCATCTCTAAATAAATGTTTTAAAAAT

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FIGURE 139

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57039

><subunit 1 of 1, 124 aa, 1 stop

><MW: 13352, pI: 5.99, NX(S/T): 1

MELPFVTHLFLPLVFLTGLCSPFNLDEHHPRLFPGPPEAEFGYSVLQHVGGGQRWMLVGAPW
DGPSGDRRGDVYRCPVGGAHNAPCAKGHLGDYQLGNSSHPAVNMHLGMSLLETGDGGFMVS

Important features:

Signal peptide:

amino acids 1-22

Cell attachment sequence.

amino acids 70-73

N-glycosylation site.

amino acids 98-101

Integrins alpha chain proteins

amino acids 67-81

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FIGURE 140

CACAGTTCCCCACCATCACTCNTCCCATTCCTTCCAACCTTTATTTTTAGCTTGCCATTGGGA
GGGGGCAGGATGGGAGGGAAAGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGAC
TTCTCATACTGGACAGAAACCGATCAGGCATGGAACTCCCCTTCGTCACTCACCTGTTCTTG
CCCCTGGTGTTCTTGACAGGTCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCT
ATTCCCAGGGCCACCAGAAGCTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGAC
AGCGATGGATGCTGGTGGGCGCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTT
TATCGCTGCCCTGTAGGGGGGGCCCAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTA
CCAACCTGGGAAATTCATCTCATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGA
CAGATGGTGATGG

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101501 101501

FIGURE 141

AAAGTTACATTTTCTCTGGAACCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCCGCTCTAGAACA
ATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA
AAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT
ACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCCCTCAGAACCTC
TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCAGTGATCGCGCCTGGAGA
AACAGTGTACTATTCTGTGGAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTGATGTCACTGATGACATC
ACGGCCACTGTGCCATAACAACCTTCGTGTGAGGGCCACATTGGGCTCACAGACCTCAGCCTG
GAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTACCCGACCTGGGATGGAGA
TCACCAAAGATGGCTTCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC
CTTGTTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAAATGGTGAGGAGTGG
GGGTATTCCAGTGACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCCAGA
CATTCGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
GGAGAGGCCATTCCCCTGGTACTGGCCCTGTTTGCCCTTTGTTGGCTTCATGCTGATCCTTGT
GGTCGTGCCACTGTTTCGTCTGGAATAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCCGTGG
TGGTCCTCCCAGACACCTTGAAAATAACCAATTCACCCCAGAAGTTAATCAGCTGCAGAAGG
GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACTCCTCAGGGCCTGGAT
CTCATAGGTTTGCGGAAGGGCCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACC
ATGAGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTTGTCTAACAGAACAC
TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGGCTGCCACTTGCTGGCTGAGCAACC
CTGGGAAAAGTGACTTCATCCCTTCGGTCCTAAGTTTTCTCATCTGTAATGGGGGAATTACC
TACACACCTGCTAAACACACACACACAGAGTCTCTCTCTATATATACACACGTACACATAAA
TACACCCAGCACTTGCAAGGCTAGAGGGAAACTGGTGACACTCTACAGTCTGACTGATTAG
TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
GGCTTGGAGAGCCCACTTTCCCAGAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
TGTTGAGTTCACTTCAAGCCCAATGCCGGTGCAGAGGGGAATGGCTTAGCGAGCTCTACAGT
AGGTGACCTGGAGGAAGGTCACAGCCACACTGAAAATGGGATGTGCATGAACACGGAGGATC
CATGAACTACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT
GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTTGTGCTCCTTTTTTC
TGTTGGTAAAGTACAGAATTCAGCAAATAAAAAGGGCCACCCTGGCCAAAAGCGGTAAAAAA
AAAAAAAAA

FIGURE 142

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57033

<subunit 1 of 1, 311 aa, 1 stop

<MW: 35076, pI: 5.04, NX(S/T): 2

MQTFTMVLEEIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLWSPVIAPGE
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITATVPYNLRVRATLGSQTS
SILKHPFNRNSTILTRPGMEITKDGFLVIELEDLGPQFEFLVAYWRREPGAEHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVQGEAIPVLALFAFVGFMILILV
VVPLFVWKMGRLQLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation site.

amino acids 40-43 and 134-137

Tissue factor proteins.

amino acids 92-119

Integrins alpha chain proteins

amino acids 232-262

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TOSTOT-28782660

FIGURE 143

TCCTGCTGATGCACATCTGGGTTTGGCAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTCTGAATACCAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG
ATGTCACTGATGACATCACGGCCACTGTGCCATAACAACCTTTGTGTCTAGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGGCGAACCCCTTGCGGCGCAAGGG
GTTNGCGAACCCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCC
ACATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

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FIGURE 144

CCCACGCGTCCGCCCACGCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAACAGGGAGAAGA
GGCAGGAGAGGAGGAGGTGGGGAGAGCACGAAGCTGGAGGCCGACACTGAGGGAGGGCGGGA
GGAGGTGAAGAAGGAGAGAGGGGAGAAGAGGCAGGAGCTGGAAAGGAGAGAGGGAGGAGGAG
GAGGAGATGCGGGATGGAGACCTGGAGTTAGGTGGCTTGGGAGAGCTTAATGAAAAGAGAAC
GGAGAGGAGGTGTGGGTTAGGAACCAAGAGGTAGCCCTGTGGGCAGCAGAAGGCTGAGAGGA
GTAGGAAGATCAGGAGCTAGAGGGAGACTGGAGGGTTCCGGGAAAAGAGCAGAGGAAAGAGG
AAAGACACAGAGAGACGGGAGAGAGAAGAAGAGTGGGTTTGAAGGGCGGATCTCAGTCCCTG
GCTGCTTTGGCATTTGGGGAACCTGGGACTCCCTGTGGGGAGGAGAGGAAAGCTGGAAGTCCT
GGAGGGACAGGGTCCCAGAAGGAGGGGACAGAGGAGCTGAGAGAGGGGGGCAGGGCGTTGGG
CAGGGGTCCCTCGGAGGCCTCCTGGGGATGGGGGCTGCAGCTCGTCTGAGCGCCCCCTCGAGC
GCTGGTACTCTGGGCTGCACTGGGGGCAGCAGCTCACATCGGACCAGCACCTGACCCCGAGG
ACTGGTGGAGCTACAAGGATAATCTCCAGGGAACTTCGTGCCAGGGCCTCCTTTCTGGGGC
CTGGTGAATGCAGCGTGGAGTCTGTGTGCTGTGGGGAAGCGGCAGAGCCCCGTGGATGTGGA
GCTGAAGAGGGTTCTTTATGACCCCTTTCTGCCCCCATTAAGGCTCAGCACTGGAGGAGAGA
AGCTCCGGGGAACCTTGTACAACACCGGCCGACATGTCTCCTTCCTGCCTGCACCCCGACCT
GTGGTCAATGTGTCTGGAGGTCCCTCCTTTACAGCCACCGACTCAGTGAAGTGC GGCTGCT
GTTTGGAGCTCGCGACGGAGCCGGCTCGGAACATCAGATCAACCACCAGGGCTTCTCTGCTG
AGGTGCAGCTCATTCACTTCAACCAGGAACTCTACGGGAATTTAGCGCTGCCTCCCGCGGC
CCCAATGGCCTGGCCATTCTCAGCCTCTTTGTCAACGTTGCCAGTACCTCTAACCCATTCTC
CAGTCGCCTCCTTAACCGCGACACCATCACTCGCATCTCCTACAAGAATGATGCCTACTTTC
TTCAAGACCTGAGCCTGGAGCTCCTGTTCCCTGAATCCTTCGGCTTCATCACCTATCAGGGC
TCTCTCAGCACCCCGCCCTGCTCCGAGACTGTCACCTGGATCCTCATTGACCGGGCCCTCAA
TATCACCTCCCTTCAGATGCACTCCCTGAGACTCCTGAGCCAGAATCCTCCATCTCAGATCT
TCCAGAGCCTCAGCGGTAACAGCCGGCCCCCTGCAGCCCTTGGCCACAGGGCACTGAGGGGC
AACAGGGACCCCCGGCACCCCGAGAGGCGCTGCCGAGGCCCCCAACTACCGCCTGCATGTGGA
TGGTGTCCCCCATGGTCGCTGAGACTCCCTTCGAGGATTGCACCCGCCCGTCTTAAGCCTC
CCCACAAGGCGAGGGGAGTTACCCCTAAAACAAAGCTATTAAAGGGACAGAATACTTA

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FIGURE 145

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34353

<subunit 1 of 1, 328 aa, 1 stop

<MW: 36238, pI: 9.90, NX(S/T): 3

MGAAARLSAPRALVLWAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLC
AVGKRQSPVDVELKRVLYDPFLPPLRLSTGGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPL
LYSHRLSELRLLLFGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSL
FVNVASTSNPFLSRLNLRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSSTPPCSE
TVTWILIDRALNITSLQMHSRLLSQNPPSQIFQSLSGNSRPLQPLAHRALRGNRDPRHPER
RCRGPNYRLHVDGVPHGR

Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 177-199

N-glycosylation site.

amino acids 118-121, 170-173 and 260-263

Eukaryotic-type carbonic anhydrases proteins

amino acids 222-270, 128-164 and 45-92

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FIGURE 146

GGCGCCTGGTTCTGCGCGTACTGGCTGTACGGAGCAGGAGCAAGAGGTGCGCCGCCAGCCTCCGCCGCCGAGCCTC
 GTTCGTGTCCCCGCCCTCGCTCCTGCAGTACTGCTCAGAAACGCTGGGGCGCCACCCTGGCAGACTAACGAA
 GCAGTCCCTTCCCACCCCAACTGCAGGTCTAATTTTGGACGCTTTGCCTGCCATTTCTTCCAGGTTGAGGGAGC
 CGCAGAGGCGGAGGCTCGCGTATTCTTGCAGTCAGCACCCACGTGCGCCCCGACGCTCGGTGCTCAGGCCCTTC
 GCGAGCGGGGCTCTCCGTCTGCGGTCCCTTGTGAAGGCTCTGGGCGGCTGCAGAGGCCGGCCGCTCCGGTTTGGCT
 CACCTCTCCCAGGAACTTCACACTGGAGAGCCAAAAGGAGTGGAAGAGCCTGTCTTGGAGATTTTCTGGGGAA
 ATCCTGAGGTCAATTCATTATGAAGTGTACCGCGCGGGAGTGGCTCAGAGTAACCACAGTGTCTTTCATGGCTAGA
 GCAATTCAGCCATGGTGGTTCCTCAATGCCACTTTATTGGAGAACTTTTGGAAAAATACATGGATGAGGATGGT
 GAGTGGTGGATAGCCAAACAACGAGGGAAAAGGGCCATCACAGACAATGACATGCAGAGTATTTTGGACCTTCAT
 AATAAATTACGAAGTCAGGTGTATCCAACAGCCTCTAATATGGAGTATATGACATGGGATGTAGAGCTGGAAAGA
 TCTGCAGAATCCTGGGCTGAAAGTTGCTTGTGGGAACATGGACCTGCAAGCTTGTCTCCATCAATTGGACAGAAT
 TTGGGAGCACACTGGGGAAGATATAGGCCCCCGACGTTTTCATGTACAATCGTGGTATGATGAAGTGAAGACTTT
 AGCTACCCATATGAACATGAATGCAACCCATATTGTCCATTAGGTGTTCTGGCCCTGTATGTACACATTATACA
 CAGGTGCTGTGGGCAACTAGTAACAGAATCGGTTGTGCCATTAATTTGTGTCAATAACATGAACATCTGGGGGCGAG
 ATATGGCCCAAAGCTGTCTACCTGGTGTGCAATTACTCCCCAAAGGGAACTGGTGGGGCCATGCCCTTACAAA
 CATGGGCGGCCCTGTTCTGCTTGCCACCTAGTTTTTGGAGGGGGCTGTAGAGAAAATCTGTGCTACAAAGAAGGG
 TCAGACAGGTATTATCCCCCTCGAGAAGAGGAAACAAATGAAATAGAACGACAGCAGTCACAAGTCCATGACACC
 CATGTCCGGACAAGATCAGATGATAGTAGCAGAAATGAAGTCATAAGCGCACAGCAAATGTCCCAAATTGTTTCT
 TGTGAAGTAAGATTAAGAGATCAGTGCAAAGGAACAACCTGCAATAGGTACGAATGTCTGTGGCTGTTTGGAT
 AGTAAAGCTAAAGTTATTGGCAGTGTACATTATGAAATGCAATCCAGCATCTGTAGAGCTGCAATTCATTATGGT
 ATAATAGACAATGATGGTGGCTGGGTAGATATCACTAGACAAGGAAGAAAGCATTATTTTCATCAAGTCCAATAGA
 AATGGTATTCAAACAATTGGCAAATATCAGTCTGCTAATTCCTTACAGTCTCTAAAGTAACAGTTTCAGGCTGTG
 ACTTGTGAAACAACCTGTGGAACAGCTCTGTCCATTTTCATAAGCCTGCTTCACATTGCCCCAAGAGTATACTGTCCT
 CGTAACTGTATGCAAGCAAATCCACATTATGCTCGTGTAAATGGAACTCGAGTTTATTCTGATCTGTCCAGTATC
 TGCAGAGCAGCAGTACATGCTGGAGTGGTTGCAAAATCACGGTGGTTATGTTGATGTAATGCCTGTGGACAAAAGA
 AAGACCTACATTGCTTCTTTTCAGAAATGGAATCTTCTCAGAAAGTTTACAGAATCCTCCAGGAGGAAAGGCATT
 AGAGTGTGTTGCTGTTGTGTGAAGTGAATACTTGGAAAGAGGACCATAAAGACTATTCCAAATGCAATATTTCTGA
 ATTTTGTATAAACTGTAACATTACTGTACAGAGTACATCAACTATTTTTCAGCCCCAAAAGGTGCCAAATGCATA
 TAAATCTTGATAAACAAAAGTCTATAAAATAAAACATGGGACATTAGCTTTGGGAAAAGTAATGAAAATATAATGG
 TTTTAGAAATCCTGTGTTAAATATTGCTATATTTTCTTAGCAGTTATTTCTACAGTTAATTACATAGTCATGATT
 GTTCTACGTTTTCATATATTATATGGTGTCTTTGTATATGCCACTAATAAAATGAATCTAAACATTGAATGTGAATG
 GCCCTCAGAAAATCATCTAGTGCATTTAAAAATAATCGACTCTAAACTGAAAGAAACCTTATCACATTTTCCCC
 AGTTCAATGCTATGCCATTACCAACTCCAAATAATCTCAAATAATTTTCCACTTAATAACTGTAAAGTTTTTTTC
 TGTTAATTTAGGCATATAGAATATTAAATTCGATATTGCACTTCTTATTTTATATAAAATAATCCTTTAATATC
 CAAATGAATCTGTTAAATGTTTGTATTCCTTGGGAATGGCCTTAAAAATAAATGTAATAAAGTCAGAGTGGTGGT
 ATGAAAACATTCTAGTGATCATGTAGTAAATGTAGGGTTAAGCATGGACAGCCAGAGCTTCTATGTACTGTTA
 AAATTGAGGTCACATATTTTCTTTTGTATCCTGGCAAATACTCCTGCAGGCCAGGAAGTATAATAGCAAAAAGTT
 GAACAAAGATGAACATAATGTATTACATTGCCACTGATTTTTTTTTTAAATGGTAAATGACCTTGTATATAA
 ATATTGCCATATCATGGTACCTATAATGGTGTATATTTGTTTCTATGAAAAATGTATTGTGCTTTGATACTAAA
 AATCTGTAAAATGTTAGTTTGGTAAATTTTTTTCTGCTGGTGGATTTACATATTAAATTTTTTCTGCTGGTGG
 TAAACATTAAATTAATCATGTTTCAAAAAAAAAAAAAA

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FIGURE 147

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45417

<subunit 1 of 1, 500 aa, 1 stop

<MW: 56888, pI: 8.53, NX(S/T): 2

MKCTAREWLRVTTVLFMARAI PAMVVPNATLLEKLLEKYMDEDEGEWWIAKQRGKRAITDNDM
QSILDLHNKLRSQVYPTASNMEYMTWDVELERSAESWAESCLWEHGPASLLPSIGQNLGAHW
GRYRPPTFHVQSWYDEVKDFSYPYEHECNPYCPFRCSGPVCTHYTQVVWATSNRIGCAINLC
HNMNIWGQIWPKAVYLVLCNYSKGNWWGHAPYKHGRPCSACPPSFGGGCRENLCYKEGSDRY
YPPREEETNEIERQQSQVHDTHVRTRSDSSRNEVISAQQMSQIVSCEVRLRDQCKGTTTCNR
YECPAGCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITRQGRKHFIKSNRNGI
QTIGKYQSANSFTVSKVTVQAVTCETTVEQLCPFHKPASHCPRVYCPRNCMQANPHYARVIG
TRVYSDLSSICRAAVHAGVVNRNHGGYVDVMPVDKRKTYIASFQNGIFSESLQNPPGGKAFRV
FAVV

Important features:

Signal peptide:

amino acids 1-20

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 protein

amino acids 165-186, 196-218, 134-146, 96-108 and 58-77

N-glycosylation site

amino acids 28-31

FIGURE 148

GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGGCG
CAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCTGGGT
GGCGTCTCCGGGCGCGCTCCGACGGGCGCAGCGCCCTCCCCATGTCCCTGCTCCACGCGG
CGCCCCCTCCGGTCAGCATGAGGCTCCTGGCGGCGCGCTGCTCCTGCTGCTGCTGGCGCTGT
ACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTAC
AGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGTTAT
CATCACCACCAAGAGCGTGTCCAGGTACCGAGGTGAGGAGCACTGCCTGCACCCCAAGCTGC
AGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGGTCTACGAA
GAATTAGGGTGAAAAACCTCAGAAGGGGAAAACCTCAAACCAGTTGGGAGACTTGTGCAAAGGA
CTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCCTTTC
TTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAAGCACTTTTTACCAACGGTCAG
TTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGATGGGAGACCCATCTCTCTTGTGCT
CCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGGGGAAAACCTCATGCCTTTCCTTTTTAA
AAAATGCTTTTTTGTATTTGTCCATACGTCACTATACATCTGAGCTTTATAAGCGCCCGGGA
GGAACAATGAGCTTGGTGGACACATTTCAATTGCAGTGTTGCTCCATTCCTAGCTTGGGAAGC
TTCCGCTTAGAGGTCTGGCGCCTCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCG
GTCACAGCCTCAGTGTGACTCCACAGTGGCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCT
CTGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCT
GGTTAATTTTTTACACACCCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAATGATC
CTTAAAGAAGGTGTGGGGTCTTTCCCAACCTGAGGATTTCTGAAAGGTTACAGGTTCAATA
TTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAACT
TAAAAATATATGAATACATGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAA
AACCTTCAAAGCATGTTTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATAT
TTGTGATTCCCATGTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTCGAAAGCTAAGAT
GACCATGCGCCCTTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCCC
CAGTATATGCCGCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCAT
TGCATGCAGGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAA
AAAAAAAAAA

09978187.101501

FIGURE 149

MSLLPRRAPPVSMRLLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPH
CEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNWNEKRRVYEE

Signal sequence:

amino acids 1-34

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FIGURE 150

GCCCCAGGGACTGCTATGGCTTCCTTTGTTGTTACCCCCGGTCTGCGTCAATGTTAAACTCCAATGTCCTCCTGTG
GTTAACTGCTCTTGCCATCAAGTTCACCCCTCATTGACAGCCAAGCACAGTATCCAGTTGTCAACACAAATTATGG
CAAAATCCGGGGCCCTAAGAACACCGTTACCCAATGAGATCTTGGGTCCAGTGGAGCAGTACTTAGGGGTCCCCTA
TGCCCTACCCCCCACTGGAGAGAGGCGGTTTCAGCCCCCAGAACCCCGTCCTCCTGGACTGGCATCCGAAATAC
TACTCAGTTTGTCTGTGTGCCCCCAGCACCTGGATGAGAGATCCTTACTGCATGACATGCTGCCCCATCTGGTT
TACCGCCAATTTGGATACTTTGATGACCTATGTTCAAGATCAAAATGAAGACTGCCTTTACTTAAACATCTACGT
GCCCCACGGAAGATGGAGCCAACACAAAGAAAAACGCAGATGATATAACGAGTAATGACCGTGGTGAAGACGAAGA
TATTCATGATCAGAACAGTAAGAAGCCCCGTCTATGTTTATATCCATGGGGGATCTTACATGGAGGGCACC GGCAA
CATGATTGACGGCAGCATTTTGGCAAGCTACGGAAACGTCTATCGTGATCACCATTAACTACCGTCTGGGAATACT
AGGGTTTTTTAAGTACCGGTGACCAGGCAGCAAAAGGCAACTATGGGCTCCTGGATCAGATTCAAGCACTGCGGTG
GATTGAGGAGAATGTGGGAGCCTTTGGCGGGGACCCCAAGAGAGTGACCATCTTTGGCTCGGGGGCTGGGGCCTC
CTGTGTGTCAGCCTGTTGACCCTGTCCCCTACTCAGAAGGTCTCTTCCAGAAGGCCATCATTAGAGCGGCACCGC
CCTGTCCAGCTGGGCAGTGAACCTACCAGCCGGCCAAGTACACTCGGATATTGGCAGACAAGGTGCGCTGCAACAT
GCTGGACACCACGGACATGGTAGAATGCCTGCGGAACAAGAACTACAAGGAGCTCATCCAGCAGACCATCACCCC
GGCCACCTACCACATAGCCTTCGGGCGGGTGATCGACGGCGACGTCTCCAGACGACCCCCAGATCCTGATGGA
GCAAGGCGAGTTCCCTCAACTACGACATCATGCTGGGCGTCAACCAAGGGGAAGGCCTGAAGTTCTGTCAGCGCAT
CGTGGATAACGAGGACGGTGTGACGCCCCAACGACTTTGACTTCTCCGTGTCCAACCTTCGTGGACAACCTTTACGG
CTACCCTGAAGGGAAAGACACTTTGCGGGAGACTATCAAGTTCATGTACACAGACTGGGCCGATAAGGAAAACCC
GGAGACGCGGGCGGAAAACCTGGTGGCTCTCTTTACTGACCACAGTGGGTGGCCCCCGCGTGGCCGCGGACCT
GCACGCGCAGTACGGCTCCCCCACCTACTTCTATGCCTTCTATCATCACTGCCAAAGCGAAATGAAGCCAGCTG
GGCAGATTCCGGCCCATGGTGATGAGGTCCCCTATGTCTTCGGCATCCCCATGATCGGTCCCACCGAGCTCTTCAG
TTGTAACTTTTTCAAGAACGACGTCTATGCTCAGCGCCGTGGTTCATGACCTACTGGACGAACCTTCGCCAAAACCTGG
TGATCCAAATCAACCAGTTTCTCAGGATACCAAGTTTCATTCACACAAAACCCCAACCGCTTTGAAGAAGTGGCCTG
GTCCAAGTATAATCCCAAAGACCAGCTCTATCTGCATATTGGCTTGAAACCCAGAGTGAGAGATCACTACCGGGC
AACGAAAGTGGCTTTCTGGTTGGAACCTCGTTCCTCATTGTCACAACCTGAACGAGATATTCCAGTATGTTTCAAC
AACCACAAAGGTTTCTCCACCAGACATGACATCATTTCCCTATGGCACCCGGCGATCTCCCGCCAAGATATGGCC
AACCACCAAACGCCCAGCAATCACTCCTGCCAACAATCCCAAACACTCTAAGGACCCTCACAAAACAGGGCCTGA
GGACACAACCTGTCTCATTGAAACCAAACGAGATTATTCACCGAATTAAGTGTACCATTGCCGTGGGGCGTC
GCTCCTCTTCTCAACATCTTAGCTTTTGCGGCGCTGTACTACAAAAGGACAAGAGGCGCCATGAGACTCACAG
GCGCCCCAGTCCCCAGAGAAACACCACAAATGATATCGCTCACATCCAGAACGAAGAGATCATGTCTCTGCAGAT
GAAGCAGCTGGAACACGATCACGAGTGTGAGTGGTGCAGGCACACGACACACTGAGGCTCACCTGCCCGCCAGA
CTACACCCTCACGCTGCGCCGGTGCAGATGACATCCCACTTATGACGCCAAACACCATCACCATGATTCCAAA
CACACTGACGGGGATGCAGCCTTTGCACACTTTTAAACCTTCAGTGGAGGACAAAACAGTACAAATTTACCCCA
CGACATTTCCACCCTAGAGTATAGCTTTGCCCCTATTTCCCTTCCCTATCCCTCTGCCCTACCCGCTCAGCAACAT
AGAAGAGGGGAAGGAAGAGAGAAGGAAGAGAGAGAGAAAGTCTCCAGACCAGGAATGTTTTTGTCCCCT
GACTTAAGACAAAAATGCAAAAAGGCAGTCATCCCATCCCGGCAGACCCTTATCGTTGGTGTGTTTTCCAGTATTAC
AAGATCAACTTCTGACCCTGTGAAATGTGAGAAGTACACATTTCTGTGTTAAATAACTGCTTTAAGATCTCTACCA
CTCCAATCAATGTTTGTGTGATAGGACATCACCATTTCAAGGCCCGGGTGTTCCTCAACGTATGGAAGCAGCT
GACACTTCTGAACTCAGCCAAGGACACTTGATATTTTTTAATTACAATGGAAGTTTAAACATTTCTTTCTGTGC
CACACAATGGATGGCTCTCCTTAAGTGAAGAAAGAGTCAATGAGATTTTGCCAGCACATGGAGCTGTAATCCAG
AGAGAAGGAAACGTAGAAATTTATTATTAAAGAATGGACTGTGCAGCGAAATCTGTACGGTCTGTGCAAGAG
GTGTTTTGCCAGCCTGAACATATTTAAGAGACTTTGT

FIGURE 151

MLNSNVLLWLTALAIKFTLIDSQAQYPVVNTNYGKIRGLRTPLPNEILGPVEQYLGVPYASP
PTGERRFQPPEPPSSWTGIRNTTQFAAVCPQHLDERSLLHDMPLIWFTANLDTLMTYVQDQN
EDCLYLNIYVPTEDGANTKKNADDITSNDRGEDEDIHDQNSKKPVMVYIHGGSYMEGTGNMI
DGSILASYGNVIVITINYRLGILGFLSTGDQAAKGNYGLLDQIQALRWIEENVGAFGGDPKR
VTIFGSGAGASCVSLLTLSHYSEGLFQKAI IQSGTALSSWAVNYQPAKYTRILADKVGCMNL
DTTDMVECLRNKNYKELIQQTITPATYHIAFGPVIDGDVIPDDPQILMEQGEFLNYDIMLGV
NQGEGLKFVDGIVDNEDGVTPNDFDFSVSNFVDNLYGYPEGKDTLRETIKFMYTDWADKENP
ETRRKTLVALFTDHQWVAPAVAADLHAQYGSPTYFYAFYHHCQSEMKPSWADSAHGDEVPIV
FGIPMIGPTELFSCNFSKNDVMLS AVVMTYWTNFAKTGDPNQVPQDTKFIHTKPNRFEEVA
WSKYNPKDQLYLHIGLKPRVRDHYRATKVAFWLELVPHLHNLNEIFQYVSTTTKVPPDMS
FPYGTRRSPAKIWPTTKRPAITPANNPKHSDPHKTGPEDTTVLIETKRDYSTEISVTI AVG
ASLLFLNILAFAALYYKKDKRRHETHRRPSPQRNTTNDIAHIQNEEIMSLQMKQLEHDHECE
SLQAHDTLRLTCPPDYTLTLRRSPDDIPLMTPNTITMIPNTLTGMQPLHTFNTFSGGQNSTN
LPHGHSTTRV

Signal sequence:

amino acids 1-24

Transmembrane domains:

amino acids 189-204, 675-692

FIGURE 152

GGGAAAGATGGCGGCGACTCTGGGACCCCTTGGGTCTGTCAGCAGTGGCGGCGATGTTTGT
CGGCTCGGGATGGGTCCAGGATGTTACTCCTTCTTCTTTTGTGGGGTCTGGGCAGGGGCCA
CAGCAAGTCGGGGCGGGTCAAACGTTTCGAGTACTTGAAACGGGAGCACTCGCTGTCTGAAGCC
CTACCAGGGTGTGGGCACAGGCAGTTCCTCACTGTGGAATCTGATGGGCAATGCCATGGTGA
TGACCCAGTATATCCGCCTTACCCAGATATGCAAAGTAAACAGGGTGCCTTGTGGAACCGG
GTGCCATGTTTCTGAGAGACTGGGAGTTGCAGGTGCACTTCAAATCCATGGACAAGGAAA
GAAGAATCTGCATGGGGATGGCTTGGCAATCTGGTACACAAAGGATCGGATGCAGCCAGGGC
CTGTGTTTGGAAACATGGACAAATTTGTGGGGCTGGGAGTATTTGTAGACACCTACCCCAAT
GAGGAGAAGCAGCAAGAGCGGGTATTCCCCTACATCTCAGCCATGGTGAACAACGGCTCCCT
CAGCTATGATCATGAGCGGGATGGGCGGCCTACAGAGCTGGGAGGCTGCACAGCCATTGTCC
GCAATCTTCATTACGACACCTTCTTGGTGATTCTGCTACGTCAAGAGGCATTTGACGATAATG
ATGGATATTGATGGCAAGCATGAGTGGAGGGACTGCATTGAAGTGCCCGGAGTCCGCCTGCC
CCGCGGCTACTACTTCGGCACCTCCTCCATCACTGGGGATCTCTCAGATAATCATGATGTCA
TTTCTTGAAGTTGTTTGAAGTACAGTGGAGAGAACCCAGAGAGGAAAAGCTCCATCGA
GATGTGTTCTTGCCCTCAGTGGACAATATGAAGCTGCCTGAGATGACAGCTCCACTGCCGCC
CCTGAGTGGCCTGGCCCTCTTCTCATCGTCTTTTTCTCCCTGGTGTTTTCTGTATTTGCCA
TAGTCATTGGTATCATACTCTACAACAAATGGCAGGAACAGAGCCGAAAGCGCTTCTACTGA
GCCCTCCTGCTGCCACCACTTTTGTGACTGTCACCCATGAGGTATGGAAGGAGCAGGCACTG
GCCTGAGCATGCAGCCTGGAGAGTGTTCTTGTCTCTAGCAGCTGGTTGGGGACTATATTCTG
TCACTGGAGTTTTGAATGCAGGGACCCCGCATTCCTCATGGTTGTGCATGGGGACATCTAACT
CTGGTCTGGGAAGCCACCCACCCAGGGCAATGCTGCTGTGATGTGCCTTTCCCTGCAGTCC
TTCCATGTGGGAGCAGAGGTGTGAAGAGAATTTACGTGGTTGTGATGCCAAAATCACAGAAC
AGAATTTTCATAGCCCAGGCTGCCGTGTTGTTTGACTCAGAAGGCCCTTCTACTTCAGTTTTG
AATCCACAAAGAATTAAAACTGGTAACACCACAGGCTTTCTGACCATCCATTCTGTTGGGT
TTGCATTTGACCCAACCCTCTGCCTACCTGAGGAGCTTTCTTTGGAAACCAGGATGGAACT
TCTTCCCTGCCTTACCTTCTTTTCACTCCATTCAATTGTCCTCTCTGTGTGCAACCTGAGCTG
GGAAAGGCATTTGGATGCCTCTCTGTTGGGGCCTGGGGCTGCAGAACACACCTGCGTTTCAC
TGGCCTTCATTAGGTGGCCCTAGGGAGATGGCTTTCTGCTTTGGATCACTGTTCCCTAGCAT
GGGTCTTGGGTCTATTGGCATGTCCATGGCCTTCCCAATCAAGTCTCTTCAGGCCCTCAGTG
AAGTTTGGCTAAAGGTTGGTGTAATAATCAAGAGAAGCCTGGAAGACATCATGGATGCCATG
GATTAGCTGTGCAACTGACCAGCTCCAGGTTTGATCAAACCAAAGCAACATTTGTCATGTG
GTCTGACCATGTGGAGATGTTTCTGGACTTGCTAGAGCCTGCTTAGCTGCATGTTTTGTAGT
TACGATTTTTGGAATCCCACTTTGAGTGCTGAAAGTGTAAGGAAGCTTTCTTCTTACACCTT
GGGCTTGGATATTGCCAGAGAAGAAATTTGGCTTTTTTTTTCTTAATGGACAAGAGACAGT
TGCTGTTCTCATGTTCCAAGTCTGAGAGCAACAGACCCTCATCATCTGTGCCTGGAAGAGTT
CACTGTCAATTGAGCAGCACAGCCTGAGTGCTGGCCTCTGTCAACCCTTATTCCACTGCCTTA
TTTGACAAGGGGTTACATGCTGCTCACCTTACTGCCCTGGGATTAAATCAGTTACAGGCCAG
AGTCTCCTTGGAGGGCCTGGAACCTCTGAGTCCTCCTATGAACCTCTGTAGCCTAAATGAAAT
TCTTAAATCACCGATGGAACCAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCG
ACCTGCAGTAGGGATAACAGGGTAATAAGCTTGGCCGCCATGG

0978187.101501

FIGURE 153

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50911

><subunit 1 of 1, 348 aa, 1 stop

><MW: 39711, pI: 8.70, NX(S/T): 1

MAATLGPLGSWQQWRRCLSARDGSRMLLLLLLLGSGQGPQQVGAGQTFEYLKREHSLSKPYQ
GVGTGSSSLWNLMGNAMVMTQYIRLTPDMQSKQALWNRVPCFLRDWELQVHFKIHGQGKKN
LHGDGLAIWYTKDRMQPGPVFGNMDKFVGLGVFVD TYPNEEKQQERVFPYISAMVNNGSLSY
DHERDGRPTELGGCTAIVRNLHYDTFLVIRYVKRHLTIMMDIDGKHEWRDCIEVPGVRLPRG
YYFGTSSITGDLSDNHDVISLKL FELTVERTPEEEKLHRDVFLPSVDNMKLPENTAPLPPLS
GLALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRKRFY

Signal sequence:

amino acids 1-38

Transmembrane domain:

amino acids 310-329

09978187-101501
TOSTOT 28782660

FIGURE 154

CCGAGCCGGGCGCGCAGCGACGGAGCTGGGGCCGGCCTGGGACCATGGGCGTGAGTGCAATCTACGGATCAGTCT
 CTGATGGTGGGTCTGTTAACTCAGTGGGGACTCCAAGATTTCCATGAAGAAAATCAGTTGTCTTCATTCAAGAAT
 TGGGGTCTGGCTCAGAAATTCCTGCAGCTGGTGAAATCTGTTTTCTAGAAGAGGTTTAATTAATGCCTGCAGTCT
 GACATGTTCCCGATTTGAGGTGAAACCATGAAGAGAAAATAGAATACTTAATAATGCTTTTCCGCAACCGCTTCT
 TGCTGCTGCTGGCCCTGGCTGCGCTGCTGGCCTTTGTGAGCCTCAGCCTGCAGTTCTTCCACCTGATCCCGGTGT
 CGACTCCTAAGAATGGAATGAGTAGCAAGAGTCGAAAGAGAATCATGCCCGACCCTGTGACGGAGCCCCCTGTGA
 CAGACCCCGTTTTATGAAGCTCTTTTGTACTGCAACATCCCCAGTGTGGCCGAGCGCAGCATGGAAGGTCATGCCC
 CGCATCATTTTTAAGCTGGTCTCAGTGCATGTGTTTATTGCCACGGAGACAGGTACCCACTGTATGTCATTCCCA
 AAACAAAGCGACAGAAATTGACTGCACTCTGGTGGCTAACAGGAAACCGTATCACCCAAAACCTGGAAGCTTTCA
 TTAGTCACATGTCAAAAGGATCCGGAGCCTCTTTTCGAAAGCCCCCTTGAACCTCCTTGCCCTCTTACCCAAATCACC
 CATTGTGTGAGATGGGAGAGCTCACACAGACAGGAGTTGTGCAGCATTTCAGAAACGGTCAGCTGCTGAGGGATA
 TCTATCTAAAGAAACACAACTCCTGCCAATGATTGGTCTGCAGACCAGCTCTATTTAGAGACCACTGGGAAAA
 GCCGGACCCTACAAAGTGGGCTGGCCTTGCTTTATGGCTTTCTCCAGATTTTGACTGGAAGAAGATTTATTTCA
 GGCACCAGCCAAGTGCCTGTTCTGCTCTGGAAGCTGCTATTGCCCGGTAAGAAACAGTATCTGGAAGAGGAGC
 AGCGTCGTAGTACCTCCTACGTTTGAAAAACAGCCAGCTGGAGAAGACCTACGGGGAGATGGCCAAGATCGTGG
 ATGTCCCCACCAAGCAGCTTAGAGCTGCCAACCCCATAGACTCCATGCTCTGCCACTTCTGCCACAATGCCGCT
 TTCCCTGTACCAGAAATGGCTGTGTTGACATGGAGCACTTCAAGGTAATTAAGACCCATCAGATCGAGGATGAAA
 GGGAAAGACGGGAGAAGAAATTGTACTTCGGGTATTCTCTCCTGGGTGCCACCCCATCCTGAACCAAACCATCG
 GCCGGATGCAGCGTGCCACCCGAGGGCAGGAAAGAAGAGCTCTTGCCCTCTACTCTGCTCATGATGTCACTCTGT
 CACCAGTTCTCAGTGCCTTGGGCCTTTTCAAGCCAGGTTCCCAAGGTTTGAGCCAGGTTGATCTTTGAGCTTT
 GGCAAGACAGAGAAAAGCCCAGTGAACATTCGGTCCGGATTCTTTACAATGGCGTCGATGTCACATTCCACACCT
 CTCTCTGCCAAGACCACCAAGCGTTCTCCCAAGCCCATGTGCCCGCTTGAAAACCTTGGTCCGCTTTGTGAAAG
 GGGACATGTTTGTAGCCCTGGGTGGCAGTGGTACAAATTATTATGATGCATGTACAGGGAAGGATTCTAAAAGG
 TATGCAGTACAGCAGTATAGAATCCATGCCAATACAGAGCATAGGGAAAGGTCCACTTCTAGTTTTGTCTGTTAC
 TAAGGGTAGAAGATTATTGCTTTTTTAAAGGCTAAATATTGTTTTGTGGGAACACAGATGGTTGGGGTTGAACAGT
 AAGCACATTGCTGCAATGTGGTACGTGAATTGCTTGGTACAAAATGGCCAGTTTACAGAGGAATAGAAGGTACTT
 TATCATAGCCAGACTTCGCTTAGAATGCCAGAATAATATAGTTCAAGACCTGAAGTTGCCAATCCAAGTTTGCAC
 TCTTCTGGCCTGCCCATGTTACTATGTGATGGAACCAGCACACCTCAACCAAATTTTTTAAATCTTAGACATT
 TTTACCTTGTCCTTGTTAAGAATTTCTTGAAGTGATTTATCTAAAATAAAGGTTGGCAAACCTTTTTCTGTAAAGG
 GCCAGATTGTAAATATTTTCAAGTGTGTGGACCAAAGGCCACATACAGTCTCTGTCTATACTACTCAACTCTGT
 TTCTGAAGCAGGAAAGCCACCACAGACAGTACATAAAGGAATATGTGTAGCTGGGTTCCAGGCCAGACAAAACA
 GATGGTGACCAGACTTGGCCCTGGGCTGTAGTTTGCTGACCCCTCATCTAAAAAATAGGCTATACTACAATTGC
 ACTTCCAGCACTTTGAGAACGAGTTGAATACCAAGAATTATTCAATGGTTCCTCCAGTAACCTCTGCTAGAAACA
 CAGAATTTGGTCTGTATCTGACACTAGAACAAAACCTTGAGGGTAAATAAACATTGAATTAGAATGAATCATAGAA
 AACTGATTAGAAGAATACTTGATGTTTATGATGATTGTGGTACAAGATAGTTTTTAAGTATGTTCTAAATATTTGT
 CTGCTGTAGTCTATTTGCTGTATATGCTGAAATTTTTGTATGCCATTTAGTATTTTTTATAGTTTAGGAAAAATATT
 TTCTAAGACCAGTTTTTAGATGACTCTTATTCCTGTAGTAATATTCAATTTGCTGTACCTGCTTGGTGGTTAGAAG
 GAGGCTAGAAGATGAATTCAGGCACCTTTCTTCCAATAAAAACTAATTATGGCTCATTCCCTTTGACAAGCTGTAGA
 ACTGGATTCATTTTTAAACATTTTCATCAGTTTCAAATGGTAAATTCGATTGATTTTTTAAATGCGTTTTTGGG
 AGAATTTTGTATTAGGTAGTTTACAGATCTTTATAAGGTGTTTTATATATTAGAAGCAATTATAATTACATCTG
 TGATTTCTGAACATAATGGTGCTAATTACAGAGAAATGGAAAGTGAAAGTGAGATTCTCTGTTGTATCGGCATTCC
 AACTTTTTCTCTTTGTTTTTGTCCAGTGTTCATTTGAATATGTCTGTTTCTATAAATAAATTTTTTAAGAATAA

09978187 101501

FIGURE 155

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48329

><subunit 1 of 1, 480 aa, 1 stop

><MW: 55240, pI: 9.30, NX(S/T): 2

MLFRNRFLLLLALALAALLAFVSLSLQFFHLIPVSTPKNGMSSKSRKRIMPDPVTEPPVTDPVY
EALLYCNIPPSVAERSMEGHAPHHFKLVSVHVFIRHGDRYPLYVIPKTKRPEIDCTLVANRKP
YHPKLEAFISHMSKSGSGASFESPLNSLPLYPNHPLCEMGELTQTGVVQHLQNGQLLRDIYLK
KHKLLPNOWSADQLYLETTGKSRTLQSGLALLYGFLPDFDWKKIYFRHQPSALFCSGSCYCP
VRNQYLEKEQRRQYLLRLKNSQLEKTYGEMAKIVDVPTKQLRAANPIDSMMLCHFCHNVSFPC
TRNGCVDMEHFKVIKTHQIEDERERREKKLYFGYSLLGAHPILNQTIGRMQRATEGRKEELF
ALYSAHDVTLSPVLSALGLSEARFPRFAARLIFELWQDREKPSEHSVRILYNGVDVTFHTSF
CQDHHKRSPKPMCPLENLVRVFVKRDMFVALGGSGTNYDACHREGF

Signal sequence:

amino acids 1-18

09978187-101501

[illegible]

AAACTCTATCTCA

FIGURE 157

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48306

><subunit 1 of 1, 916 aa, 1 stop

><MW: 100204, pI: 4.92, NX(S/T): 4

MIPARLHRDYKGLVLLGILLGTLWETGCTQIRYSVP EELEKGSRVGDISRDLGLEPRELAER
GVRIIPRGRTQLFALNPRSGSLVTAGRIDREELCMGAIKCQLNLDILMEDKVKIYGVEVEVR
DINDNAPYFRESELEIKISENAATEMRFP LPHAWDPDIGKNSLQSYELSPNTHFSLIVQNGA
DGSKYPELV LKRALDREEKAAHHLVLTASDGGDPVRTGTARIRVMVLDANDNAPAFAPQPEYR
ASVPENLALGTQLLVVNATDPDEGVNAEVRYSFRYVDDKAAQVFKLDCNSGTISTIGELDHE
ESGFYQMEVQAMDNAGYSARAKVLITVLDVNDNAPEVVLTSLASSVPENSPRGTLIALLNVN
DQDSEENGQVICFIQGNLPFKLEKSYGNYYSLVTDIVLDREQVPSYNITVTATDRGTPPLST
ETHISLNVADTNDNPPVFPQASYSAYIPENNPRGVSLSVSTAHPDCEENAQITYSLAENTI
QGASLSSYVSINSDTGVLIALSSFDYEQFRDLQVKVMARDNGHPPLSSNVSLSLFVLDQNDN
APEILYPALPTDGSTGVELAPRSAEPGYLVTKVAVDRDSGQNAWLSYRLLKASEPGLFSVG
LHTGEVRTARALLDRDALKQSLVVAVQDHGQPPLSATVTTLTVAVADSIPQVLADLGSLESPA
NSETSDLTLYLVVAVAAVSCVFLAFVILLALLRLRRWHKSRLQASGGGLTGAPASHFVGVD
GVQAF LQTY SHEVSLTTDSRKSHLIFPQPNYADMLVSQESFEKSEPLLLSGDSVFSKDSHGL
IEVSLYQIFFLFFFNCSV SQAGVQRYDHSSLRPQTPRLKQLSHLCLRCNRDYRCKPPTVCLS
IYLSIYLSIYLSIYLLLSCTDGSLTPVIPVLWEAEAGGSPEVGSLRPA

Signal sequence:

amino acids 1-30

Transmembrane domains:

amino acids 693-711, 809-823, 869-888

FIGURE 158

CCCAGGCTCTAGTGCAGGAGGAGAAGGAGGAGGAGCAGGAGGTGGAGATTCCCAGTTAAAAG
GCTCCAGAATCGTGTACCAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTCCGAA
TCAGTAGGTGACCCCGCCCTGGATTCTGGAAGACCTCACCATGGGACGCCCCGACCTCGT
GCGGCCAAGACGTGGATGTTCTTGCTCTTGCTGGGGGGAGCCTGGGCAGGACACTCCAGGGC
ACAGGAGGACAAGGTGCTGGGGGGTTCATGAGTGCCAACCCCATTCGCAGCCTTGGCAGGCGG
CCTTGTTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTTGTAGGTGGCAACTGGGTCCTT
ACAGCTGCCCACTGTAAAAAACCGAAATACACAGTACGCCTGGGAGACCACAGCCTACAGAA
TAAAGATGGCCCAGAGCAAGAAATACCTGTGGTTTCAGTCCATCCCACACCCCTGCTACAACA
GCAGCGATGTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCATCC
CTGGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTGGCCAGAAGTG
CACCGTCTCAGGCTGGGGCACTGTCACCAGTCCCCGAGAGAATTTTCTGACACTCTCAACT
GTGCAGAAGTAAAAATCTTTCCCCAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACA
GATGGCATGGTCTGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCCAGGGCGATTCTGGAGG
CCCCCTGGTGTGTGATGGTGCCTCCAGGGCATCACATCCTGGGGCTCAGACCCCTGTGGGA
GGTCCGACAAACCTGGCGTCTATACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGATC
ATAGGCAGCAAGGGCTGATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACTCT
CTGGTTC

099787-101501

FIGURE 159

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48336

<subunit 1 of 1, 260 aa, 1 stop

<MW: 28048, pI: 7.87, NX(S/T): 1

MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVL
VGGNWVLTAAHCKKPKYTVRLGDHSLQNKDGPEQEIPVVQSI PHPCYNSSDVEDHNHDLMLL
QLRDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCED
AYPGQITDGMVCAGSSSKGADTCQGDGGPLVCDGALQGITSWGSDPCGRSDKPGVYTNI CRY
LDWIKKIIGSKG

Important Features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 51-71

N-glycosylation site.

amino acids 110-113

Serine proteases, trypsin family, histidine active site.

amino acids 69-74 and 207-217

Tyrosine kinase phosphorylation site.

amino acids 182-188

Kringle domain proteins motif

amino acids 205-217

09978187-101501

FIGURE 160

GGCGCCGGTGCACCGGGCGGGCTGAGCGCCTCCTGCGGCCCGGCCTGCGCGCCCCGGCCCCG
CGCGCCGCCACGCCCCAACCCCGGCCCGCGCCCCCTAGCCCCCGCCGGGCCCGCGCCCCG
GCCCCGCGCCAGGTGAGCGCTCCGCCCCGCGGAGGCCCGCCCCGGCCCCGCCCCCGCCCCG
CCCCGGCCGGCGGGGGAACCGGGCGGATTCTCGCGCGTCAAACCACCTGATCCATAAAAC
ATTCATCCTCCCGGCGGCCCGCGCTGCGAGCGCCCCGCCAGTCCGCGCCGCGCCCGCCCTCG
CCCTGTGCGCCCTGCGCGCCCTGCGCACCCGCGGCCCGAGCCAGCCAGAGCCGGGCGGAGC
GGAGCGCGCCGAGCCTCGTCCCGCGGCCGGGCGGGGCCGGGCCGTAGCGGCGGCGCCTGGA
TGCGGACCCGGCCGCGGGGAGACGGGCGCCCCGCCCGAAACGACTTTCAGTCCCCGACGCGC
CCCGCCCAACCCCTACGATGAAGAGGGCGTCCGCTGGAGGGAGCCGGCTGCTGGCATGGGTG
CTGTGGCTGCAGGCCTGGCAGGTGGCAGCCCCATGCCAGGTGCCTGCGTATGCTACAATGA
GCCCAAGGTGACGACAAGCTGCCCCAGCAGGGCCTGCAGGCTGTGCCCCGTGGGCATCCCTG
CTGCCAGCCAGCGCATCTTCCTGCACGGCAACCGCATCTCGCATGTGCCAGCTGCCAGCTTC
CGTGCCCTGCCGCAACCTCACCATCCTGTGGCTGCACTCGAATGTGCTGGCCCCGAATTGATGC
GGCTGCCTTCACTGGCCTGGCCCTCCTGGAGCAGCTGGACCTCAGCGATAATGCACAGCTCC
GGTCTGTGGACCCTGCCACATTCCACGGCCTGGGCCGCCTACACACGCTGCACCTGGACCGC
TGCGGCCTGCAGGAGCTGGGCCCGGGGCTGTTCCGCGGCCTGGCTGCCCTGCAGTACCTCTA
CCTGCAGGACAACGCGCTGCAGGCACTGCCTGATGACACCTTCCGCGACCTGGGCAACCTCA
CACACCTCTTCCTGCACGGCAACCGCATCTCCAGCGTGCCCCGAGCGCGCCTTCCGTGGGCTG
CACAGCCTCGACCGTCTCCTACTGCACCAGAACCGCGTGGCCCATGTGCACCCGCATGCCTT
CCGTGACCTTGGCCGCCTCATGACACTCTATCTGTTTGCCAACAATCTATCAGCGCTGCCCA
CTGAGGCCCTGGCCCCCTGCGTGCCCTGCAGTACCTGAGGCTCAACGACAACCCCTGGGTG
TGTGACTGCCGGGCACGCCCCACTCTGGGCCTGGCTGCAGAAGTTCGCGGGCTCCTCCTCCGA
GGTGCCCTGCAGCCTCCCGCAACGCCTGGCTGGCCGTGACCTCAAACGCCTAGCTGCCAATG
ACCTGCAGGGCTGCGCTGTGGCCACCGGCCCTTACCATCCCATCTGGACCGGCAGGGCCACC
GATGAGGAGCCGCTGGGGCTTCCCAAGTGCTGCCAGCCAGATGCCGCTGACAAGGCCTCAGT
ACTGGAGCCTGGAAGACCAGCTTCGGCAGGCAATGCGCTGAAGGGACGCGTGCCGCCCGGTG
ACAGCCCGCCGGGCAACGGCTCTGGCCCAACGGCACATCAATGACTCACCCCTTTGGGACTCTG
CCTGGCTCTGCTGAGCCCCCGCTCACTGCAGTGCGGCCCGAGGGCTCCGAGCCACCAGGGTT
CCCCACCTCGGGCCCTCGCCGGAGGCCAGGCTGTTACGCAAGAACCGCACCCGCAGCCACT
GCCGTCTGGGCCAGGCAGGCAGCGGGGTGGCGGGACTGGTGACTCAGAAGGCTCAGGTGCC
CTACCCAGCCTCACCTGCAGCCTCACCCCCCTGGGCCTGGCGCTGGTGCTGTGGACAGTGCT
TGGGCCCTGCTGAACCCCCAGCGGACACAAGAGCGTGCTCAGCAGCCAGGTGTGTGTACATAC
GGGGTCTCTCTCCACGCCGCCAAGCCAGCCGGGCGGCCGACCCGTGGGGCAGGCCAGGCCAG
GTCCTCCCTGATGGACGCTGCGGCCCGCCACCCCCATCTCCACCCCATCATGTTTACAGGG
TTCGGCGGCAGCGTTTGTTCAGAACGCCGCTCCACCCAGATCGCGGTATATAGAGATAT
GCATTTTATTTTACTTGTGTAAAAATATCGGACGACGTGGAATAAAGAGCTCTTTTCTTAAA
AAAA

FIGURE 161

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44184

><subunit 1 of 1, 473 aa, 1 stop

><MW: 50708, pI: 9.28, NX(S/T): 6

MKRASAGGSRL LAWVLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRI
FLHG NRISHVPAASFRACRNLTILWLHSNVLARIDAAFTGLALLEQLDLSDNAQLRSVDPA
TFHGLGRLHTLHLDRCLQELGPGLFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLH
GNRISSVPERAFRGLHSLDRLLHLHQN RVAHVHPHAFRDLGRLMTLYLFANNLSALPTEALAP
LRALQYLRLNDNPWVCD CRARPLWAWLQKFRGSSSEVP CSLPQRLAGRDLKRLAANDLQGCA
VATGPYHPIWTGRATDEEPLGLPKCCQPD AADKASVLEPGRPASAGNALKGRVPPGDSPPGN
GSGPRHINDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLGQA
GSGGGGTGDSEGS GALPSLTCSLTPLGLALVLWTVLGPC

Important features:

Signal peptide:

amino acids 1-26

Leucine zipper pattern.

amino acids 135-156

Glycosaminoglycan attachment site.

amino acids 436-439

N-glycosylation site.

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

VWFC domain

amino acids 411-425

FIGURE 162

GGAAGTCCACGGGGAGCTTGGATGCCAAAGGGAGGACGGCTGGGTCTCTGGAGAGGACTAC
TCACTGGCATATTTCTGAGGTATCTGTAGAATAACCACAGCCTCAGATACTGGGGACTTTAC
AGTCCCACAGAACCGTCTCTCCAGGAAGCTGAATCCAGCAAGAACAATGGAGGCCAGCGGGA
AGCTCATTTGCAGACAAAGGCAAGTCTTTTTTCTCTTTCTCCTTTTGGGCTTATCTCTGGCG
GGCGCGGCGGAACCTAGAAGCTATTCTGTGGTGGAGGAACTGAGGGCAGCTCCTTTGTCAC
CAATTTAGCAAAGGACCTGGGTCTGGAGCAGAGGGAATTCTCCAGGCGGGGGGTAGGGTTG
TTTCCAGAGGGGAACAACTACATTTGCAGCTCAATCAGGAGACCGCGGATTTGTTGCTAAAT
GAGAAATTGGACCGTGAGGATCTGTGCGGTACACAGAGCCCTGTGTGCTACGTTTCCAAGT
GTTGCTAGAGAGTCCCTTCGAGTTTTTTCAAGCTGAGCTGCAAGTAATAGACATAAACGACC
ACTCTCCAGTATTTCTGGACAAACAAATGTTGGTGAAAGTATCAGAGAGCAGTCTCCTGGG
ACTACGTTTCTCTGAAGAATGCCGAAGACTTAGATGTAGGCCAAAACAATATTGAGAACTA
TATAATCAGCCCCAACTCCTATTTTCGGGTCTCACCCGCAAACGCAGTGATGGCAGGAAAT
ACCCAGAGCTGGTGCTGGACAAAGCGCTGGACCGAGAGGAAGAAGCTGAGCTCAGGTTAACA
CTCACAGCACTGGATGGTGGCTCTCCGCCCAGATCTGGCACTGCTCAGGTCTACATCGAAGT
CCTGGATGTCAACGATAATGCCCTGAATTTGAGCAGCCTTTCTATAGAGTGCAGATCTCTG
AGGACAGTCCGGTAGGCTTCTGGTGTGTAAGGTCTCTGCCACGGATGTAGACACAGGAGTC
AACGGAGAGATTTCTATTCACTTTTCCAAGCTTCAGAAGAGATTGGCAAAACCTTTAAGAT
CAATCCCTTGACAGGAGAAATTGAACTAAAAAAACAACCTCGATTTCGAAAACTTCAGTCCT
ATGAAGTCAATATTGAGGCAAGAGATGCTGGAACCTTTTCTGGAAAATGCACCGTTCTGATT
CAAGTGATAGATGTGAACGACCATGCCCCAGAAGTTACCATGTCTGCATTTACCAGCCCAAT
ACCTGAGAACGCGCCTGAAACTGTGGTTGCACTTTTCAGTGTTTCAGATCTTGATTAGGAG
AAAATGGGAAAATTAGTTGCTCCATTAGGAGGATCTACCCTTCTCCTGAAATCCGCGGAA
AACTTTTACACCCTACTAACGGAGAGACCACTAGACAGAGAAAGCAGAGCGGAATACAACAT
CACTATCACTGTCACTGACTTGGGGACCCCTATGCTGATAACACAGCTCAATATGACCGTGC
TGATCGCCGATGTCAATGACAACGCTCCCGCCTTCACCCAAACCTCCTACACCCTGTTCTGTC
CGCGAGAACAACAGCCCCGCCCTGCACATCCGCAGCGTCAGCGCTACAGACAGAGACTCAGG
CACCAACGCCCAGGTACCTACTCGCTGCTGCCGCCCCAGGACCCGCACCTGCCCTCACAT
CCCTGGTCTCCATCAACGCGGACAACGGCCACCTGTTCTGCCCTCAGGTCTCTGGACTACGAG
GCCCTGCAGGGGTTCCAGTTCGCGCTGGGCGCTTCAGACCACGGCTCCCCGGCGCTGAGCAG
CGAGGCGCTGGTGCGCTGGTGGTGCTGGACGCCAACGACAACCTCGCCCTTCGTGCTGTACC
CGCTGCAGAACGGCTCCGCGCCCTGCACCGAGCTGGTGCCCCGGGCGGCCGAGCCGGGCTAC
CTGGTGACCAAGGTGGTGGCGGTGGACGGCGACTCGGGCCAGAACGCCTGGCTGTCTGTACCA
GCTGCTCAAGGCCACGGAGCTCGGTCTGTTCTGGCGTGTGGGCGCACAAATGGCGAGGTGCGCA
CCGCCAGGCTGCTGAGCGAGCGCGACGCGGCCAAGCACAGGCTGGTGGTGCTGGTCAAGGAC
AATGGCGAGCCTCCGCGCTCGGCCACCGCCACGCTGCACGTGCTCCTGGTGGACGGCTTCTC
CCAGCCCTACCTGCCTCTCCCGGAGGCGGCCCCGACCCAGGCCAGGCCGACTTGCTCACCG
TCTACCTGGTGGTGGCGTTGGCCTCGGTGTCTTCGCTCTTCTCTTTTCGGTGCTCCTGTTT
GTGGCGGTGCGGCTGTGTAGGAGGAGCAGGGCGGCCTCGGTGGGTGCTGCTGGTGCCCGA
GGGCCCCCTTCCAGGGCATCTTGTGGACATGAGCGGCACCAGGACCCTATCCAGAGCTACC
AGTATGAGGTGTGTCTGGCAGGAGGCTCAGGGACCAATGAGTTCAAGTTCCTGAAGCCGATT
ATCCCCAACTTCCCTCCCAGTGCCCTGGGAAAGAAATACAAGGAAATTCTACCTTCCCCAA
TAACTTTGGGTTCATATTCAGTGAACCATAGTTGACTTTTACATTCCATAGGTATTTTATT
TGTGGCATTTCATGCCAATGTTTATTTCCCCCAATTTGTGTGTATGTAATATTGTACGGAT
TACTCTTGATTTTTCTCATGTTCTTTCTCCCTTTGTTTTAAAGTGAACATTTACCTTTATT
CCTGGTCTT

FIGURE 163

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48314

<subunit 1 of 1, 798 aa, 1 stop

<MW: 87552, pI: 4.84, NX(S/T): 5

MEASGKLICRQRQVLFSFLLLGLSLAGAAEPRSYSVVEETEGSSFVTNLAKDLGLEQREFSR
RGVRVVSARGNKLHLQLNQETADLLLNEKLDREDLCGHTEPCVLRQVLLESPEFFQAEQV
IDINDHSPVFLDKQMLVKVSESSPPGTTFPLKNAEDLDVGQNNIENYIISPNSYFRVLTRKR
SDGRKYPELVLDKALDREEEAELRLTLTALDGGSPPRSGTAQVYIEVLDVNDNAPEFEQPFY
RVQISEDSPVGFLVVKVSATDVDTGVNGEISYSLFQASEEIGKTFKINPLTGEIELKKQLDF
EKLQSYEVNIEARDAGTFSGKCTVLIQVIDVNDHAPEVTMSAFTSPIPENAPETVVALFSVS
DLDSGENGKISCISIQEDLPFLLKSAENFYTLLTERPLDRESRAEYNITITVTDLGTPMLITQ
LNMTVLIADVNDNAPAFQTQTSYTLFVRENNSPALHIRSVSATDRDSGTNAQVTYSLPPQDP
HLPLTSLVSINADNGHLFALRSLDYEALQGFQFRVGASDHGSPALSSEALVRVVVLDANDNS
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATELGFGVWAH
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHVLLVDGFSQPYLPLPEAAPTQAA
ADLLTVYLVVALASVSSLFVLLFVAVRLCRRSRAASVGRCLVPEGPLPGHLVDMMSGTRT
LSQSYQYEVCLAGGSGTNEFKFLKPIIPNFPPQCPGKEIQGNSTFPNNFGFNIQ

Important features:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 685-712

Cadherins extracellular repeated domain signature.

amino acids 122-132, 231-241, 336-346, 439-449 and 549-559

ATP/GTP-binding site motif A (P-loop).

amino acids 285-292

N-glycosylation site.

amino acids 418-421, 436-439, 567-570 and 786-789

FIGURE 164

ACCCACGCGTCCGCCCACGCGTCCGCCCACGCGTCCGCCCACGCGTCCGCGCGTAGCCGTGC
GCCGATTGCCTCTCGGCCTGGGCAATGGTCCCGGCTGCCGGTCGACGACCGCCCCGCGTCAT
GCGGCTCCTCGGCTGGTGGCAAGTATTGCTGTGGGTGCTGGGACTTCCCGTCCGCGGCGTG
AGGTTGCAGAGGAAAGTGGTCGCTTATGGTCAGAGGAGCAGCCTGCTCACCTCTCCAGGTG
GGGGCTGTGTACCTGGGTGAGGAGGAGCTCCTGCATGACCCGATGGGCCAGGACAGGGCAGC
AGAAGAGGCCAATGCGGTGCTGGGGCTGGACACCCAAGGCGATCACATGGTGATGCTGTCTG
TGATTCTTGGGGAAGCTGAGGACAAAGTGAGTTCAGAGCCTAGCGGCGTCACCTGTGGTGCT
GGAGGAGCGGAGGACTCAAGGTGCAACGTCCGAGAGAGCCTTTTCTCTCTGGATGGCGCTGG
AGCACACTTCCCTGACAGAGAAGAGGAGTATTACACAGAGCCAGAAGTGGCGGAATCTGACG
CAGCCCCGACAGAGGACTCCAATAACACTGAAAGTCTGAAATCCCCAAAGGTGAACTGTGAG
GAGAGAAACATTACAGGATTAGAAAATTTCACTCTGAAAATTTTAAATATGTCACAGGACCT
TATGGATTTTCTGAACCCAAACGGTAGTGACTGTACTCTAGTCCTGTTTTACACCCCGTGGT
GCCGCTTTTCTGCCAGTTTGGCCCCCTCACTTTAACTCTCTGCCCCGGGCATTTCCAGCTCTT
CACTTTTTGGCACTGGATGCATCTCAGCACAGCAGCCTTTCTACCAGGTTTGGCACCGTAGC
TGTCCTAATATTTTATTATTTCAAGGAGCTAAACCAATGGCCAGATTTAATCATAACAGATC
GAACACTGGAAACACTGAAAATCTTCATTTTTAATCAGACAGGTATAGAAGCCAAGAAGAAT
GTGGTGGTAACTCAAGCCGACCAAATAGGCCCTCTTCCCAGCACTTTGATAAAAAGTGTGGA
CTGGTTGCTTGTATTTTCCTTATTCTTTTTAATTAGTTTTATTATGTATGCTACCATTCGAA
CTGAGAGTATTCGGTGGCTAATTCCAGGACAAGAGCAGGAACATGTGGAGTAGTGATGGTCT
GAAAGAAGTTGGAAAGAGGAACTTCAATCCTTCGTTTCAGAAATTAGTGCTACAGTTTCATA
CATTTTCTCCAGTGACGTGTTGACTTGAACTTCAGGCAGATTAAAAGAATCATTTGTTGAA
CAACTGAATGTATAAAAAAATTATAAACTGGTGTTTTAACTAGTATTGCAATAAGCAAATGC
AAAAATATTCAATAG

FIGURE 165

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48333

><subunit 1 of 1, 360 aa, 1 stop

><MW: 39885, pI: 4.79, NX(S/T): 7

MVPAAGRRPVRMRLLGWWQVLLWVLGLPVRGVEVAEESGRLWSEEQPAHPLQVGAVYLGEE
ELLHDPMGQDRAAEEANAVLGLDTQGDHVMVLSVIPGEAEDKVSSEPSGVTCGAGGAEDSRC
NVRESLFSLDGAGAHFPDREEEYYTEPEVAESDAAPTEDSNNTESLKSPKVNCEERNITGLE
NFTLKILNMSQDLMDFLNPNGSDCTLVLFYTPWCRFSASLAPHFNSLPRAFPALHFLALDAS
QHSSLSTRFGTVAVPNILLFQGAKPMARFNHTDRTLETCLKIFIFNQTGIEAKKNVVVTQADQ
IGPLPSTLIKSDWLLVFSLFFLISFIMYATIRTESIRWLIPGQEQEHVE

Important features:

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 321-340

Homologous region to dilsufide isomerase

amino acids 212-302

N-glycosylation site.

amino acids 165-168, 181-184, 187-190, 194-197, 206-209, 278-281
and 293-296

Thioredoxin domain

amino acids 211-227

FIGURE 166

CCCGGCTCCGCTCCCTCTGCCCCCTCGGGGTCGCGCGCCACGATGCTGCAGGGCCCTGGCT
CGCTGCTGCTGCTCTTCCTCGCCTCGCACTGCTGCCTGGGCTCGGCGCGCGGGCTCTTCCTC
TTTGGCCAGCCCGACTTCTCCTACAAGCGCAGCAATTGCAAGCCCATCCCGGTCAACCTGCA
GCTGTGCCACGGCATCGAATACCAGAACATGCGGGCTGCCAACCTGCTGGGCCACGAGACCA
TGAAGGAGGTGCTGGAGCAGGCCGGCGCTTGGATCCCGCTGGTCATGAAGCAGTGCCACCCG
GACACCAAGAAGTTCCTGTGCTCGCTCTTCGCCCCCGTCTGCCTCGATGACCTAGACGAGAC
CATCCAGCCATGCCACTCGCTCTGCGTGACGGTGAAGGACCGCTGCGCCCCGGTCATGTCCG
CCTTCGGCTTCCCCTGGCCCCGACATGCTTGAGTGCGACCGTTTCCCCCAGGACAACGACCTT
TGCATCCCCCTCGCTAGCAGCGACCACCTCCTGCCAGCCACCGAGGAAGCTCCAAAGGTATG
TGAAGCCTGCAAAAATAAAAATGATGATGACAACGACATAATGGAAACGCTTTGTAAAAATG
ATTTTGCACTGAAAATAAAAGTGAAGGAGATAACCTACATCAACCGAGATACCAAAATCATC
CTGGAGACCAAGAGCAAGACCATTTACAAGCTGAACGGTGTGTCCGAAAGGGACCTGAAGAA
ATCGGTGCTGTGGCTCAAAGACAGCTTGCAGTGACCTGTGAGGAGATGAACGACATCAACG
CGCCCTATCTGGTCATGGGACAGAAACAGGGTGGGGAGCTGGTGATCACCTCGGTGAAGCGG
TGGCAGAAGGGGCAGAGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCAGTGCTA
GTCCCCGGCATCCTGATGGCTCCGACAGGCCTGCTCCAGAGCACGGCTGACCATTTCTGCTCC
GGGATCTCAGCTCCCGTTCCCCAAGCACACTCCTAGCTGCTCCAGTCTCAGCCTGGGCAGCT
TCCCCCTGCCTTTTGCACGTTTGCATCCCCAGCATTTCTGAGTTATAAGGCCACAGGAGTG
GATAGCTGTTTTACCTAAAGGAAAAGCCCACCCGAATCTTGTAGAAATATTCAAACCTAATA
AAATCATGAATATTTTAA

FIGURE 167

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50920

><subunit 1 of 1, 295 aa, 1 stop

><MW: 33518, pI: 7.74, NX(S/T): 0

MLQGPGSLLLLFLASHCCLGSARGLFLFGQPDFS YKRSNCKPIPVNLQLCHGIEYQNMRLPN
LLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAPVCLDDLDETIQPCHS LCVQVKDR
CAPVMSAFGFPWPDMLECDRFPQDNDLCIPLASSDHLLPATEEAPKVCEACKKNDDNDIM
ETLCKNDFALKIKVKEITYINRDTKIILETKSKTIYKLNGVSE RDLKKSVLWLKDSLQCTCE
EMNDINAPYLVMGQKQG GELVITSVKRWQKGQREFKRISRSIRKLQC

Important features:

Signal peptide:

amino acids 1-20

Cysteine rich domain, homologous to frizzled N terminus

amino acids 6-153

09978187-101501
TOSTOT-282660

FIGURE 168

GTGGAGGCCCGCCGACGATGGCGGGGCGGACGGAGGCCGAGACGGGGTTGGCCGAGCCCCGGG
CCCTGTGCGCGCAGCGGGGCCACCGCACCTACGCGCGCCGCTGGGTGTTCTTGCTCGCGATC
AGCCTGCTCAACTGCTCCAACGCCACGCTGTGGCTCAGCTTTGCACCTGTGGCTGACGTCAT
TGCTGAGGACTTGGTCCTGTCCATGGAGCAGATCAACTGGCTGTCACTGGTCTACCTCGTGG
TATCCACCCCATTTGGCGTGGCGGCCATCTGGATCCTGGACTCCGTGCGGGCTCCGTGCGGCG
ACCATCCTGGGTGCGTGGCTGAACTTTGCCGGGAGTGTGCTACGCATGGTGCCCTGCATGGT
TGTTGGGACCCAAAACCCATTTGCCTTCTCATGGGTGGCCAGAGCCTCTGTGCCCTTGCCC
AGAGCCTGGTCATCTTCTCTCCAGCCAAGCTGGCTGCCTTGTGGTTCCCAGAGCACCAGCGA
GCCACGGCCAACATGCTCGCCACCATGTCTGAACCTCTGGGCGTCTTGTGGCCAATGTGCT
GTCCCCTGTGCTGGTCAAGAAGGGTGAGGACATTCCGTTAATGCTCGGTGTCTATACCATCC
CTGCTGGCGTCGTCTGCCTGCTGTCCACCATCTGCCTGTGGGAGAGTGTGCCCCCACCCTG
CCCTCTGCCGGGGCTGCCAGCTCCACCTCAGAGAAGTTCTTGATGGGCTCAAGCTGCAGCT
CATGTGGAACAAGGCCTATGTCATCCTGGCTGTGTGCTTGGGGGGAATGATCGGGATCTCTG
CCAGCTTCTCAGCCCTCCTGGAGCAGATCCTCTGTGCAAGCGGCCACTCCAGTGGGTTTTCC
GGCCTCTGTGGCGCTCTCTTCATCACGTTTGGGATCCTGGGGGCACTGGCTCTCGGCCCTA
TGTGGACCGGACCAAGCACTTCACTGAGGCCACCAAGATTGGCCTGTGCCTGTTCTCTCTGG
CCTGCGTGCCCTTTGCCCTGGTGTCCCAGCTGCAGGGACAGACCCTTGCCCTGGCTGCCACC
TGCTCGCTGCTCGGGCTGTTTGGCTTCTCGGTGGGCCCCGTGGCCATGGAGTTGGCGGTCTGA
GTGTTCTTCCCCGTGGGGGAGGGGGCTGCCACAGGCATGATCTTTGTGCTGGGGCAGGCCG
AGGGAATACTCATCATGCTGGCAATGACGGCACTGACTGTGCGACGCTCGGAGCCGTCCTTG
TCCACCTGCCAGCAGGGGGAGGATCCACTTGACTGGACAGTGTCTCTGCTGCTGATGGCCGG
CCTGTGCACCTTCTTCAGCTGCATCCTGGCGGTCTTCTTCCACACCCCATACCGGCGCCTGC
AGGCCGAGTCTGGGGAGCCCCCTCCACCCGTAACGCCGTGGGCGGCGCAGACTCAGGGCCG
GGTGTGGACCGAGGGGGAGCAGGAAGGGCTGGGGTCTGGGGCCAGCACGGCGACTCCGGA
GTGCACGGCGAGGGGGGCTCGCTAGAGGACCCAGAGGGCCCGGAGCCCCCACCAGCCT
GCCACCGAGCGACTCCCCGTGCGCAAGGCCAGCAGCCACCGACGCGCCCTCCCGCCCCGGC
AGACTCGCAGGCAGGGTCCAAGCGTCCAGGTTTATTGACCCGGCTGGGTCTCACTCCTCCTT
CTCCTCCCCGTGGGTGATCACGTAGCTGAGCGCCTTGTAAGTCCAGGTTGCCCGCCACATCGA
TGGAGGCGAACTGGAACATCTGGTCCACCTGCGGGCGGGGGCGAAAGGGCTCCTTGCGGGCT
CCGGGAGCGAATTACAAGCGCGCACCTGAAAA

FIGURE 169

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50988

><subunit 1 of 1, 560 aa, 1 stop

><MW: 58427, pI: 6.86, NX(S/T): 2

MAGPTEAETGLAEPRALCAQRGHRITYARRWVFLLAISLLNCSNATLWLSFAPVADVIAEDLV
LSMEQINWLSLVYLVVSTPFGVAAIWILDSVGLRAATILGAWLNFAGSVLRMVPCMVVGTQN
PFAFLMGGQSLCALAQSLVIFSPAKLAALWFPEHQ RATANMLATMSNPLGVLVANVLSPLV
KKGEDIPMLGLVYTIPAGVVCLLSTICLWESVPPTPPSAGAASSTSEKFLDGLKLQLMWNKA
YVILAVCLGGMIGISASFALLEQILCASGHSSGFSGLCGALFITFGILGALALGPYVDRTK
HFTEATKIGLCFLSLACVPFALVSQ LQGQTLALAATCSLLGLFGFSVGPVAMELAVECSFPV
GEGAATGMIFVLGQAEGILIMLAMTALT VRRSEPSLSTCQQGEDPLDWTVSLLLMAGLCTFF
SCILAVFFHTPYRRLQAESGEPPSTRNAVGGADSGPGVDRGGAGRAGVLGPSTATPECTARG
ASLEDPRGPGSPHPACHRATPRAQGPAATDAPSRPGRLAGRVQASRFIDPAGSHSSFSSPWVIT

Important features:

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 61-79, 98-112, 126-146, 169-182, 201-215, 248-268,
280-300, 318-337, 341-357, 375-387, 420-441

N-glycosylation site.

amino acids 40-43 and 43-46

Glycosaminoglycan attachment site.

amino acids 468-471

FIGURE 170

GTCCACATCCTGCTCAACTGGGTGAGTCCCTCTTAGACCAGCTCTTGTCCATCATTTGCTGAAGTGGACCAAC
TAGTTCCTCCAGTAGGGGGTCTCCCTGGCAATTCTTGATCGGCGTTTGGACATCTCAGATCGCTTCCAATGAAGA
TGGCCTTGCTTGGGGTCTGCTTGTTCATAATCATCTAACTATGGGACAAGGTTGTGCCGGCAGCTCTGGGGG
AAGGAGCACGGGGCTGATCAAGCCATCCAGGAAACACTGGAGGACTTGTCCAGCCTTGAAAGAACTCTAGTGGTT
TCTGAATCTAGCCCACTTGGCGGTAAGCATGATGCAACTTCTGCAACTTCTGCTGGGGCTTTTGGGGCCAGGTGG
CTACTTATTTCTTTTAGGGGATTGTGAGGAGGTGACCACTCTCACGGTGAAATACCAAGTGTGAGAGGAAGTGCC
ATCTGGTACAGTGATCGGGAAGCTGTCCAGGAACTGGGCCGGGAGGAGAGGCGGAGGCAAGCTGGGGCCGCCTT
CCAGGTGTTGAGCTGCCTCAGGCGCTCCCCATTAGGTGGACTCTGAGGAAGGCTTGTCTCAGCACAGGCAGGCG
GCTGGATCGAGAGCAGCTGTGCCGACAGTGGGATCCCTGCTTGGTTTCTTTGATGTGCTTGCCACAGGGGATT
GGCTCTGATCCATGTGGAGATCCAAGTGTCTGGACATCAATGACCACAGCCACGGTTTCCCAAAGGCGAGCAGGA
GCTGGAAATCTCTGAGAGCGCTCTCTGCGAACCCGGATCCCCCTGGACAGAGCTCTTGACCCAGACACAGGCC
TAACACCCTGCACACCTACACTCTGTCTCCAGTGAGCACTTTCCTTGGATGTGATTGTGGGCCCTGATGAGAC
CAAACATGCAGAACTCATAGTGGTGAAGGAGCTGGACAGGGAATCCATTCAATTTTTTGATCTGGTGTTAACTGC
CTATGACAATGGGAACCCCCCAAGTCAAGTACCAGCTTGGTCAAGGTCAACGTCTTGGACTCCAATGACAATAG
CCCCTGCTTGTGAGAGTTCACTGGCACTGGAAATCCAAGAAGATGCTGCACCTGGTACGCTTCTCATAAACT
GACCGCCACAGACCTGACCAAGGCCCAATGGGGAGGTGGAGTTCTTCTCAGTAAGCACATGCCCTCCAGAGGT
GCTGGACACCTTCAGTATTGATGCCAAGACAGGCCAGGTCACTCTGCGTCGACCTCTAGACTATGAAAAGAACCC
TGCCTACGAGGTGGATGTTGAGCAAGGGACCTGGGTCCCAATCCTATCCAGCCCATTCGAAAGTTCTCATCAA
GGTTCTGGATGTCAATGACAACATCCCAAGCATCCACGTACATGGGCCTCCAGCCATCACTGGTGTCAGAAGC
TCTTCCCAAGGACAGTTTTATTGCTCTTGTCTATGGCAGATGACTTGGATTGAGGACACAATGGTTTGGTCCACTG
CTGGCTGAGCCAAGAGCTGGGCCACTTCAGGCTGAAAAGAATAATGGCAACACATACATGTTGCTAACCAATGC
CACACTGGACAGAGAGCAGTGGGCCAAATATACCTCACTCTGTTAGCCCAAGACCAAGGACTCCAGCCCTTATC
AGCCAAGAAACAGCTCAGCATTGAGATCAGTGACATCAACGACAATGCACCTGTGTTTGGAGAAAAGCAGGTATGA
AGTCTCCACGCGGGAAAACAACCTTACCTCTCTTACCTCATTACCATCAAGGCTCATGATGCAGACTTGGGCAT
TAATGGAAAAGTCTCATACCGCATCCAGGACTCCCAAGTTGCTCACTTAGTAGCTATTGACTCCAACACAGGAGA
GGTCACTGCTCAGAGGTCACTGAACTATGAAGAGATGGCCGGCTTTGAGTTCCAGGTGATCGCAGAGGACAGCGG
GCAACCCTATGCTTGCACTCCAGTGTCTGTGTGGGTGAGCCTCTTGGATGCCAATGATAATGCCCCAGAGGTGGT
CCAGCCTGTGCTCAGCGATGGAAGGCCAGCCTCTCCGTGCTTGTGAATGCCCTCCACAGGCCACCTGCTGGTGCC
CATCGAGACTCCCAATGGCTTGGGCCAGCGGGCACTGACACACCTCCACTGGCCACTCACAGCTCCCGGCCATT
CCTTTTGACAACCATTGTGGCAAGAGATGCAGACTCGGGGGCAAATGGAGAGCCCCCTCTACAGCATCCGCAATGG
AAATGAAGCCACCTCTTCATCCTCAACCTCATACGGGGCAGCTGTTTCGTCAATGTACCAATGCCAGCAGCCT
CATTGGGAGTGAGTGGGAGCTGGAGATAGTAGTAGAGGACCAGGGAAGCCCCCTTACAGACCCGAGCCCTGTT
GAGGTGCTGTTTGTACAGTGTGGACACCTGAGGGACTCAGCCCGCAAGCCTGGGGCCTTGAGCATGTGCTGAT
GCTGACGGTGTCTGCCTGGCTGTACTGTTGGGCATCTTCGGGTTGATCCTGGCTTTGTTTATGTCCATCTGCCG
GACAGAAAAGAAGGACAACAGGGCCTACAACCTGTCCGGAGGCCGAGTCCACCTACCGCCAGCAGCCCAAGAGGCC
CCAGAAACACATTGAGAAGGCAGACATCCACCTCGTGCCTGTGCTCAGGGGTGAGGAGGTGAGCCTTGTGAAGT
CGGCGAGTCCCAAAAGATGTGGACAAGGAGGCGATGATGGAAGCAGGCTGGGACCCCTGCCTGCAGGCCCTT
CCACCTCACCCCGACCTGTACAGGACGCTGCGTAATCAAGGCAACCAGGGAGCACCGGCGGAGAGCCGAGAGGT
GCTGCAAGACACGGTCAACCTCCTTTCAACCTCCAGGCAGAGGAATGCCCTCCGGGAGAACCTGAACCTTCC
CGAGCCCCAGCCTGCCACAGGCCAGCCAGCTTCCAGGCCCTTGAAGGTTGCAGGCAGCCCCACAGGGAGGCTGGC
TGGAGACCAGGGCAGTGAGGAAGCCCCACAGAGGCCACCAGCCTCCTCTGCAACCTGAGACGGCAGCGACATCT
CAATGGCAAAGTGTCCCTGAGAAAGAATCAGGGCCCCGTGAGATCCTGCGGAGCCTGGTCCGGCTGTCTGTGGC
TGCCTTCGCCGAGCGGAACCCCGTGGAGGAGCTCACTGTGGATTCTCCTCCTGTTTCAAGAAATCTCCAGCTGCT
GTCTTGTGCTCATCAGGGCCAATTCCAGCCCAACCAAAACACCGAGGAAATAAGTACTTGGCCAAGCCAGGAGG
CAGCAGGAGTGCAATCCAGACACAGATGGGCCATCTTCGGGTTGATCCTGGCTTTGTTTATGTCCATCTGCCG
AGGGCCTTTGGATCCTGAAGAGGACCTCTCTGTGAAGCAACTGTAGAGAAGAGCTGTCAAGTCTGCTGGACCC
CAGCACAGGTCTGGCCCTGGACCGGCTGAGCGCCCTGACCCGGCCTGGATGGCGAGACTCTCTTTGCCCTCAC
CACCACCTACCGTGACAATGTGATCTCCCGGATGCTGCAGCCACGGAGGAGCCGAGGACCTTCCAGACGTTCGG
CAAGGCAGAGGCACCGAGCTGAGCCCAACAGGCACGAGGCTGGCCAGCACCTTTGTCTCGGAGATGAGCTCACT
GCTGGAGATGCTGCTGGAACAGCGCTCCAGCATGCCCGTGGAGGCCGCTCCGAGGCGCTGCGGCGGCTCTCGGT
CTGCGGGAGGACCTCAGTTTAGACTTGGCCACCATGAGCTCAGGCTGAAAGTGCAAGGGGACCCAGGTGG
AAAGACGGGGAGCTGAGGGCAAGAGCAGAGGCAGCAGCAGCAGCAGGTGCTGTAACATACCTCAGACGCT
CTGGATCCAAGAACCAGGGGCTGAGGATCTGTGGAACAAGAGCTGGTTTCTAAATCTTGTAACTCACTAGCTAG
CGGCGGCTGAGAACTTTAGGGTGAAGTGTCTACCCCCACAGAGGAGGCAAGAGCCCCAGGACTAACAGCTGAC
TGACCAAAGCAGCCCCCTTGTAAAGCAGCTCTGAGTCTTTTGGAGGACAGGGACGTTTGTGGCTGAGATAAGTGT
TCCTGGCAAAACATATGTGGAGCAAAAGGGTCAGTCTCTGGCAGAACAGATGCCACGGAGTATCACAGGCAGG
AAAGGGTGGCCTTCTGGGTAGCAGGAGTCAAGGGGCTGACCTGGGGTGCCAGGAAATGCTCTGACCTAT
CAATAAAGGAAAAGCAGTAAAAA

FIGURE 171

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48331

<subunit 1 of 1, 1184 aa, 1 stop

<MW: 129022, pI: 5.20, NX(S/T): 5

MMQLLQLLLGLLGPGGYLFLLGDCQEVTTTLTVKYQVSEEVPSGTVIGKLSQELGREERRRQA
GAAFQVLQLPQALPIQVDSEEGLLSTGRRLDREQLCRQWDPCLVSFDVLATGDLALIHVEIQ
VLDINDHQPRFPKGEQELEISESASLRTRIPLDRALDPDTGPNTLHTYTLSPSEHFALDVIV
GPDETKHAELIVVKELDREIHSFFDLVLTAYDNGNPPKSGTSLVKVNVLDSDNDNSPAFAESS
LALEIQEDAAPGTTLLIKLTATDPDQGPNGEVEFFLSKHMPPEVLDTFSIDAKTGQVILRRPL
DYEKNPAYEVDVQARDLGNPIPAHCKVLIKVLVDVNDNIPSIHVTWASQPSLVSEALPKDSF
IALVMADDLDSGHNGLVHCWLSQELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLAQAQD
QGLQPLSAKKQLSIQISDINDNAPVFESRYEVSTRENNLPSLHLITIKAHDADLGINGKVS
YRIQDSPVAHLVAIDSNTGEVTAQRSLNVEEMAGFEFQVIAEDSGQPMLASSVSVWVSLDA
NDNAPEVVQPVLSGKASLSVLVNASTGHLLVPIETPNGLGPAGTDTPPLATHSSRPFLTT
IVARDADSGANGEPLYIRNGNEAHLFILNPHTGQLFVNVTNASSLIGSEWELEIIVVEDQGS
PPLQTRALLRVMFVTSVDHLRDSARKPGALSMSMLTVICLAVLLGIFGLILALFMSICRTEK
KDNRAYNCREAESTYRQQPKRPQKHIQKADIHLVPVLRGQAGEPCEVGQSHKDVDKEAMMEA
GWDPCLQAPFHLTPTLYRTLNRQGNQGAPAESREVLQDTVNLLFNHPRQRNASRENLNLEP
QPATGQPRSRPLKVAGSPTGRLAGDQGSEEAPQRPPASSATLRRQRHLNGKVSPEKESGPRQ
ILRSLVRLSVAFAERNPVEELTVDSPPVQQISQLLSLLHQGFQPKPNHRGNKYLAKEPGGS
RSAIPDTDGPSARAGGQTDPEQEEGPLDPEEDLSVKQLLEEEELSSLLDPSTGLALDRLSAPD
PAWMARLSLPLTTNYRDNVISPDAAATEEPRTFQTFGKAEAPELSPTGTRLASTFVSEMSSL
LEMLLEQRSSMPVEAASEALRRLSVCGRTLSLDLATSAAAGMKVQGDPPGGKTGTEGKSRGSS
SSSRCL

Important features:

Signal peptide:

amino acids 1-13

Transmembrane domain:

amino acids 719-739

N-glycosylation site.

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

Cadherins extracellular repeated domain signature.

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563

FIGURE 172

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGCGAGTCCCGGCTGCAGCACCTGGGAGAAGG
CAGACCGTGTGAGGGGGCCTGTGGCCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAG
GCAGGAGCCTTCCTTACACTTCGCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCT
CCCAGATACTATTTTTTTGGATTTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTAT
GAGATACGTCAGTATGTTGTACAGGTGATCTTCTCCGTGACGTTTGCATTTTCTTGCACCAT
GTTTGAGCTCATCATCTTTGAAATCTTAGGAGTATTGAATAGCAGCTCCCGTTATTTTCACT
GGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTTTTCATGGTGCCTTTTTTACATTGGC
TATTTTATTGTGAGCAATATCCGACTACTGCATAAAACAACGACTGCTTTTTTCTGTCTCTT
ATGGCTGACCTTTATGTATTTCTTCTGGAACTAGGAGATCCCTTTCCCATTTCTCAGCCCAA
AACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTGGTGTGATTGGAGTGA CTCTC
ATGGCTCTTCTTTCTGGATTTGGTGCTGTCAACTGCCCATACTTACATGTCTTACTTCTC
CAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATA
TGATCATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAA
GTGCATAACAAACCATCAGGTTTCTGGGGAATGATAAAAAGTGTTACCACTTCAGCATCAGG
AAGTGAAAATCTTACTCTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGC
TTTTTCTGGAAACAGCTGATCTATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTC
AAGGGGAAATATTTTAATTTTCTTGGTTACTTTTTCTCTATTTACTGTGTTTGGAAAATTTT
CATGGCTACCATCAATATTGTTTTTGATCGAGTTGGGAAAACGGATCCTGTCACAAGAGGCA
TTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGTGAAGTTTTGGTCCCAACACATT
TCCTTCATTCTTGTTGGAATAATCATCGTCACATCCATCAGAGGATTGCTGATCACTCTTAC
CAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCCTCCAATGTCAATTGTCCTGCTATTAGCAC
AGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCTTTAGAA
TACCGCACCATATACTGAAGTCCTTGGAGAACTGCAGTTCAACTTCTATCACCGTTGGTT
TGATGTGATCTTCCTGGTCAGCGCTCTCTCTAGCATACTCTTCCTCTATTTGGCTCACAAAC
AGGCACCAGAGAAGCAAATGGCACCTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGT
GGTTTCAAATTTAGATATAAGAGGGGGGAAAAATGGAACCAGGGCCTGACATTTTATAAAC
AAACAAAATGCTATGGTAGCATTTTTTACCTTCATAGCATACTCCTTCCCCGTCAGGTGATA
CTATGACCATGAGTAGCATCAGCCAGAACATGAGAGGGAGAACTAACTCAAGACAATACTCA
GCAGAGAGCATCCCGTGTGGATATGAGGCTGGTGTAGAGGCGGAGAGGCCAAGAACTAA
AGGTGAAAAATACACTGGAACCTCTGGGGCAAGACATGTCTATGGTAGCTGAGCCAAACACGT
AGGATTTCCGTTTTAAGGTTACATGGAAAAGGTTATAGCTTTGCCTTGAGATTGACTCAT
AAAATCAGAGACTGTAACAAAAAAGGGCGGCCGCGACTCTAGAGTCG
ACCTGCAGAAGCTTGGCCGCCATGGCCCACTTGTTTATTGCAGCTTATAATG

FIGURE 173

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEI
LGVLNSSSRYPFWKMNLCVILLILVFMVPPFYIGYFIVSNIRLLHKQRLLFSCLLWLTFMYFF
WKLGDPPILSPKHGILSIEQLISRVGVIGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDI
LALERRLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQ
QEVDAL EELSRQLFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVF
DRVGKTDVPTRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAIS
SKSSNVIVLLLAQIMGMYFVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSA
LSSILFLYLAHKQAPEKQMAP

Important features:

Signal peptide:

amino acids 1-23

Potential transmembrane domains:

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,
425-444

N-glycosylation sites.

amino acids 67-70, 180-183 and 243-246

Eukaryotic cobalamin-binding proteins

amino acids 151-160

FIGURE 174

CATGGGAAGTGGAGCCGGAGCCTTCCTTACACTCGCCATGAGTTTCCTCATCGACTCCAGCA
TCATGATTACCTCCCNGANACTATTTTTTGGATTTGGGTGGCTTTTCTTCNGCGCCAATGTT
TAAAGACTATGAGATACGTCAGTATGTTGTACNGGTGATCTTCTCCGTGACGTTTGCCATTT
CTTGCACCATGTTTTGAGCTCATCATCTTTGAAATCTTNGGAGTATTGAATAGCAGCTCCCGT
TATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTNTCATGGTGCCTTT
TTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGACTGCTTTTTT
CCTGTCTCTTATGGCTGACCTTTATGTATTTCCAG

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FIGURE 175

GTGTTGCCCTTGGGGAGGGGAAGGGGAGCCNGGCCCTTTCCTAAAATTTGGCCAAGGGTTTC
TTTNTTGAATTCGGGGTTNNGNATACCTTCCCAGAAAATATTTTTTGGATTTGGGGTAGNTT
TTTTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAGGTGATNTT
NTCCGTGACGTTTGCATTTTCTTGACCATGTTTGAGCTCATCATNTTTGAAATNTTAGGAG
TATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATC
CTGGTTTTTCATGGTGCCTTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCA
TAAACAACGACTGCTTTTTTCTGTCTNTTATGGCTGACCTTTATGTATTTNTTNTGGAAAN
TAGGAGATCCCTTTCCCATTCTC

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FIGURE 176

CTCGCGCAGGGATCGTCCCATGGCCGGGGCTCGGAGCCGCGACCCCTTGGGGGGCCTCCGGGATTTGCTACCTTTT
TGGCTCCCTGCTCGTCAACTGCTCTTCTCACGGGCTGTGCGCTTCAATCTGGACGTGATGGGTGCCTTGCGCAA
GGAGGGCGAGCCAGGCAGCCTCTTCGGCTTCTCTGTGGCCCTGCACCGGCAGTTGCAGCCCCGACCCAGAGCTG
GCTGCTGGTGGGTGCTCCCCAGGCCCTGGCTCTTCTGGGCAGCAGGCGAATCGCACTGGAGGCCTCTTCGCTTG
CCCGTTGAGCCTGGAGGAGACTGACTGCTACAGAGTGGACATCGACCAGGGAGCTGATATGCAAAGGAAAGCAA
GGAGAACCAGTGGTTGGGAGTCAGTGTTCGGAGCCAGGGGCTGGGGGCAAGATTGTTACCTGTGCACACCGATA
TGAGGCAAGGCAGCGAGTGGACCAGATCCTGGAGACGCGGGATATGATTGGTCGCTGCTTTGTGCTCAGCCAGGA
CCTGGCCATCCGGGATGAGTTGGATGGTGGGGAATGGAAGTTCTGTGAGGGACGCCCCAAGGCCATGAACAATT
TGGGTTCTGCCAGCAGGGCACAGCTGCCGCCTTCTCCCCTGATAGCCACTACCTCCTCTTTGGGGCCCCAGGAAC
CTATAATTGGAAGGGCACGGCCAGGGTGGAGCTCTGTGCACAGGGCTCAGCGGACCTGGCACACCTGGACGACGG
TCCCTACGAGGCGGGGGGAGAGAAGGAGCAGGACCCCCGCTCATCCCGGTCCCTGCCAACAGCTACTTTGGCTT
CTCTATTGACTCGGGGAAAGGTCTGGTGCCTGCAGAAGAGCTGAGCTTTGTGGCTGGAGCCCCCGCGCCAACCA
CAAGGGTGCTGTGGTCATCCTGCGCAAGGACAGCGCCAGTCGCTGGTGCCCGAGGTTATGCTGTCTGGGGAGCG
CCTGACCTCCGGCTTTGGCTACTCACTGGCTGTGGCTGACCTCAACAGTGATGGCTGGCCAGACCTGATAGTGGG
TGCCCCCTACTTCTTTGAGCGCCAAGAAGAGCTGGGGGGTGTGTGTATGTGTACTTGAACCAGGGGGGTCACTG
GGCTGGGATCTCCCTCTCCGGCTCTGCGGCTCCCTGACTCCATGTTTCGGGATCAGCCTGGCTGTCTGGGGGA
CCTCAACCAAGATGGCTTTCCAGATATTGCAGTGGGTGCCCCCTTTGATGGTGATGGGAAAGTCTTCATCTACCA
TGGGAGCAGCCTGGGGGTGTGCGCCAACCTTCACAGGTGCTGGAGGGCGAGGCTGTGGGCATCAAGAGCTTCGG
CTACTCCTGTGAGGCAGCTTGGATATGGATGGGAACCAATACCCTGACCTGCTGGTGGGCTCCCTGGCTGACAC
CGCAGTGCTCTTCAGGGCCAGACCCATCCTCCATGTCTCCATGAGGTCTCTATTGCTCCACGAAGCATCGACCT
GGAGCAGCCCAACTGTGCTGGCGGCCACTCGGTCTGTGTGGACCTAAGGGTCTGTTTCAGCTACATTGCAGTCCC
CAGCAGCTATAGCCCTACTGTGGCCCTGGACTATGTGTTAGATGCGGACACAGACCAGGCTCCGGGGCCAGGT
TCCCCGTGTGACGTTCTGAGCCGTAACCTGGAAGAACCAGCACCAGGCCTCGGGCACCCTGTGGCTGAAGCA
CCAGCATGACCGAGTCTGTGGAGACGCCATGTTCCAGCTCCAGGAAAATGTCAAAGACAAGCTTCGGGGCATTGT
AGTGACCTTGTCTACAGTCTCCAGACCCCTCGGCTCCGGCGACAGGCTCCTGGCCAGGGGCTGCCTCCAGTGGC
CCCCATCCTCAATGCCACCAGCCAGCACCAGCGGGCAGAGATCCACTTCTGAAAGCAAGGCTGTGGTGAAGA
CAAGATCTGCCAGAGCAATCTGCAGCTGGTCCACGCCCGCTTCTGTACCCGGGTGAGCGACACGGAATTCCAACC
TCTGCCCATGGATGTGGATGGAACAACAGCCCTGTTTGCAGTGGGAGCCAGTCATTGGCCCTGGAGCTGAT
GGTCACCAACCTGCCATCGGACCCAGCCAGCCAGCCAGGCTGATGGGGATGATGCCCATGAAGCCAGCTCCTGGT
CATGCTTCTGACTCACTGCACTACTCAGGGGTCCGGGCCCTGGACCCCTGCGGAGAAGCCACTCTGCCTGTCCAA
TGAGAATGCCTCCCATGTTGAGTGTGAGCTGGGGAACCCCATGAAGAGAGGTGCCAGGTACCTTCTACCTCAT
CCTTAGCACCTCCGGGATCAGCATTGAGACCACGGAACCTGGAGGTAGAGCTGCTGTTGGCCACGATCAGTGAGCA
GGAGCTGCATCCAGTCTCTGCACGAGCCCGTGTCTTATTGAGCTGCCACTGTCCATTGCAGGAATGGCCATTCC
CAGCTTTGACCCGCGGGCTGTGCTGCATGTCTGGGGCCGTCTCTGGAACAGCACCTTTCTGGAGGAGTACTCAGC
CAAGTATGAGGTACGGTTTCCAACCAAGGCCAGTCGCTCAGAACCCTGGGCTCTGCCTTCTCAACATCATGTG
GCCTCATGAGATTGCCAATGGGAAGTGGTTGCTGTACCCAATGCAGGTTGAGCTGGAGGGCGGGCAGGGGCTGG
GCAGAAAGGGCTTTGCTCTCCAGGCCCAACATCCTCCACCTGGATGTGGACAGTAGGGATAGGAGGGCGGGGA
GCTGGAGCCACCTGAGCAGCAGGAGCCTGGTGAGCGGCAGGAGCCAGCATGTCTGGTGGCCAGTGTCTCTGTC
TGAGAAGAAGAAAAACATCACCCCTGGACTGCGCCCGGGGCACGGCCAACTGTGTGGTGTTCAGCTGCCCACTCTA
CAGCTTTGACCCGCGGGCTGTGCTGCATGTCTGGGGCCGTCTCTGGAACAGCACCTTTCTGGAGGAGTACTCAGC
TGTGAAGTCCCTGGAAGTGATTGTCCGGGCCAACATCACAGTGAAGTCTCCATAAAGAACTTGATGCTCCGAGA
TGCCCTCCACAGTGATCCAGTGATGGTATACTTGGACCCCATGGCTGTGGTGGCAGAAGGAGTGGCCCTGGTGGGT
CATCCTCCTGGCTGTACTGGCTGGGCTGCTGGTGCTAGCACTGCTGGTGCTGCTCCTGTGGAAGATGGGATTCTT
CAAACGGGCGAAGCACCCCGAGGCCACCGTGCCCCAGTACCATGCGGTGAAGATTCTCGGGGAAGACCGACAGCA
GTTCAAGGAGGAGAAGACGGGCACCATCCTGAGGAACAACCTGGGGCAGCCCCCGCGGGAGGGGCCGGATGCACA
CCCCATCCTGGCTGCTGACGGGCATCCCGAGCTGGGCCCCGATGGGCATCCAGGGCCAGGCACCGCCTAGGTTCC
CATGTCCCAGCCTGGCCTGTGGCTGCCCTCCATCCCTTCCCCAGAGATGGCTCCTTGGGATGAAGAGGGTAGAGT
GGGCTGCTGGTGTGCGCATCAAGATTTGGCAGGATCGGCTTCCCTCAGGGGCACAGACCTCTCCCACCCACAAGAAC
TCCTCCCACCCAACTTCCCTTAGAGTGCTGTGAGATGAGAGTGGGTAAATCAGGGACAGGGCCATGGGGTAGGG
TGAGAAGGGCAGGGGTGTCTGATGCAAAGGTGGGGAGAAGGGATCCTAATCCCTTCTCTCCATTACCCCTGT
GTAACAGGACCCCAAGGACCTGCCCTCCCCGGAAGTGCCTTAACCTAGAGGGTCGGGGAGGAGGTTGTGTCACTGA
CTCAGGCTGCTCCTTCTAGTTTCCCCCTCATCTGACCTTAGTTTGTGCTGCCATCAGTCTAGTGGTTTCGTGGT
TTCGTCTATTTATTAATAAATATTTGAGAACAAAAA

FIGURE 177

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737

><subunit 1 of 1, 1141 aa, 1 stop

><MW: 124671, pI: 5.82, NX(S/T): 5

MAGARSRDPWGASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHRQL
QPRPQSWLLVGAPQALALPGQQANRTGGLFACPLSLEETDCYRVDIDQGADMOKESKENQWL
GVSVRSQGPGGKIVTCAHRYEARQRVDQILETRDMIGRCFVLSQDLAIRDELDDGGEWKFC
RPQGHEQFGFCQQGTAAAFSPDSHYLLFGAPGTYNWKGRTARVELCAQGSADLAHLDDGPYEA
GGEKEQDPRLIPVPANSYFGFSIDSGKGLVRAEELS FVAGAPRANHKGAVVILRKDSASRLV
PEVMLSGERLTSGFGYSLAVADLNSDGPDLIVGAPYFFERQEELGGAVYVYLNQGGHWAGI
SPLRLCGSPDSMFGISLAVLGDNLNQGFPDIAVGAPFDGDGKVFYHGS SLGVVAKPSQVLE
GEAVGIKSFYSLSGSLDMDGNQYPDLLVGS LADTAVLFRARPILHVSHEVSIAPRSIDLEQ
PNCAGGHSVCVDLRVCFSYIAVPSSYSPTVALDYVLDADTDRLRGQVPRVTFLSRNLEEPK
HQASGTVWLKHQHDRVCGDAMFQLQENVKDKLR AIVVTLSYSLQTPRLRRQAPGQGLPPVAP
ILNAHQ PSTQRAEIHFLKQCGEDKICQSNLQLVHARFCTRVSDTEFQPLPMDVDGTTALFA
LSGQPVIGLELMVTNLPSPDPAQPQADGDDAHEAQLLVMLPDSLHYS GVRALDPAEKPLCLSN
ENASHVECELGNPMKRGAQVTFYLILSTSGIS IETTELEVLELLLATISEQELHPVSARARVF
IELPLSIAGMAIPQQLFFSGVVRGERAMQSERDVGSKVKYEVT VSNQGQSLRTLGS AFLNIM
WPHEIANGKWL LYPMQVELEGGQGPQKGLCSPRPNILHLDVDSRDRRRRELEPPEQQEPGE
RQEPSMSWWPVSSAEKKKNITLDCARGTANC VVFSCPLYSFDRAAVLHVWGRLWNSTFLEEY
SAVKSLEIVVRANITVKSSIKNLMLRDASTVIPVMVYLDPM AVVAEGVPWWVILLAVLAGLL
VLALLVLLLWKMGFFKRAKHPEATVPQYH AVKIPREDRQQFKEEKTGTILRNNWGS PRREGP
DAHPI LAADGHPELGPDPGHPGPETA

Important features:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 1040-1062

N-glycosylation sites.

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

Integrins alpha chain proteins.

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408 and 1031-1047

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FIGURE 178

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGGCGCGTGCAGCAGCTCCAGA
AAGCAGCGAGTTGGCAGAGCAGGGCTGCATTTCCAGCAGGAGCTGCGAGCACAGTGCTGGCT
CACAACAAGATGCTCAAGGTGTCAGCCGTACTGTGTGTGTGTGCAGCCGCTTGGTGCAGTCA
GTCTCTCGCAGCTGCCGCGGCGGTGGCTGCAGCCGGGGGGCGGTCCGACGGCGGTAATTTTC
TGGATGATAAACAATGGCTCACCAACAATCTCTCAGTATGACAAGGAAGTCGGACAGTGGAAC
AAATTCCGAGACGAAGTAGAGGATGATTATTTCCGCACTTGGAGTCCAGGAAAACCCTTCGA
TCAGGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCGCCATAAAGTAT
GCATTGCTCAAGATTCTCAGACTGCAGTCTGCATTAGTCACCGGAGGCTTACACACAGGATG
AAAGAAGCAGGAGTAGACCATAGGCAGTGGAGGGGTCCCATATTATCCACCTGCAAGCAGTG
CCCAGTGGTCTATCCCAGCCCTGTTTGTGGTTCAGATGGTCATACCTACTCTTTTCAGTGCA
AACTAGAATATCAGGCATGTGTCTTAGGAAAACAGATCTCAGTCAAATGTGAAGGACATTGC
CCATGTCCTTCAGATAAGCCCACCAGTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCT
GGAGTTCAGGGAAGTGGCAAACAGATTGCGGGACTGGTTCAAGGCCCTTCATGAAAGTGGA
GTCAAAACAAGAAGACAAAAACATTGCTGAGGCCTGAGAGAAGCAGATTCGATACCAGCATC
TTGCCAATTTGCAAGGACTCACTTGGCTGGATGTTTAAACAGACTTGATACAAACTATGACCT
GCTATTGGACCAGTCAGAGCTCAGAAGCATTTACCTTGATAAGAATGAACAGTGTACCAAGG
CATTCTTCAATTCTTGTGACACATACAAGGACAGTTTAATATCTAATAATGAGTGGTGCTAC
TGCTTCCAGAGACAGCAAGACCCACCTTGCCAGACTGAGCTCAGCAATATTCAGAAGCGGCA
AGGGGTAAAGAAGCTCCTAGGACAGTATATCCCCCTGTGTGATGAAGATGGTTACTACAAGC
CAACACAATGTCATGGCAGTGTTGGACAGTGCTGGTGTGTTGACAGATATGGAAATGAAGTC
ATGGGATCCAGAATAAATGGTGTGAGATTGTGCTATAGATTTTGAGATCTCCGGAGATTT
TGCTAGTGGCGATTTTCATGAATGGACTGATGATGAGGATGATGAAGACGATATTATGAATG
ATGAAGATGAAATTGAAGATGATGATGAAGATGAAGGGGATGATGATGATGGTGGTGATGAC
CATGATGTATACATTTGAATTGATGACAGTTGAAATCAATAAATTCTACATTTCTAATATTTA
CAAAAATGATAGCCTATTTAAATTTATCTTCTTCCCCAATAACAAAATGATTCTAAACCTCA
CATATATTTTGTATAATTATTTGAAAAATTGCAGCTAAAGTTATAGAACTTTATGTTTAAAT
AAGAATCATTTGCTTTGAGTTTTTATATTCCTTACACAAAAGAAAATACATATGCAGTCTA
GTCAGACAAAATAAAGTTTTGAAGTGCTACTATAATAAATTTTTTCACGAGAACAACTTTGT
AAATCTTCCATAAGCAAAATGACAGCTAGTGCTTGGGATCGTACATGTTAATTTTTTTGAAAG
ATAATTCTAAGTGAAATTTAAATAAATAAATTTTTAATGACCTGGGTCTTAAGGATTTAGG
AAAAATATGCATGCTTTAATTGCATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAG
GATAACAGAGAGATACCACATGACTCCAAAAAAAAAAAAAAAAA

FIGURE 179

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49829

><subunit 1 of 1, 436 aa, 1 stop

><MW: 49429, pI: 4.80, NX(S/T): 0

MLKVSAVLCVCAAAWCSQSLAAAAVAAAGGRSDGGNFLDDKQWLTTISQYDKEVGQWNKFR
DEVEDDYFRTWSPGKPFQALDPAKDPCLKMKCSRHKVCIAQDSQTAVCISHRRLTHRMKEA
GVDHRQWRGPILSTCKQCPVVYPSPVCGSDGHTYSFQCKLEYQACVLGKQISVKCEGHCP
SDKPTSTSRNVKRACSDLEFREVANRLRDWFKALHESGSQNKTKTLLRPERSRFDTSILPI
CKDSLGMWFMNRLDTNYDLLLDQSELRSIYLDKNEQCTKAFFNSCDTYKDSLISNNEWCYCFQ
RQQDPPCQTELSNIQKRQGVKKLLGQYIPLCDEDEGYKPTQCHGSVGQCWCVDRYGNEVMGS
RINGVADCAIDFEISGDFASGDFHEWTDDEDEDEDDIMNDEDEIEDDDEDEGDDDDGGDDHDVYI

Important features:

Signal peptide:

amino acids 1-16

Leucine zipper pattern.

amino acids 246-267

N-myristoylation sites.

amino acids 357-362, 371-376 and 376-381

Thyroglobulin type-1 repeat proteins

amino acids 353-365 and 339-352

FIGURE 180

CAGACTCCAGATTTCCCTGTCAACCACGAGGAGTCCAGAGAGGAAACGCGGAGCGGAGACAACAGTACCTGACGC
CTCTTTTCAGCCCCGGGATCGCCCCAGCAGGGATGCGGCGACAAGATCTGGCTGCCCTTCCCCGTGCTCCTTCTGGCC
GCTCTGCCTCCGGTCTGCTGCCTGGGGCGCCGGCTTACACCTTCCCTCGATAGCGACTTCACCTTTACCCTT
CCCCCGGCCAGAAAGGAGTGCTTCTACCAGCCCCATGCCCTGAAGGCCTCGCTGGAGATCGAGTACCAAGTTTTA
GATGGAGCAGGATTAGATATTGATTTCCATCTTGCTCTCCAGAAGGCAAAACCTTAGTTTTGAACAAAGAAAA
TCAGATGGAGTTACACTGTAGAGACTGAAGTTGGTGATTACATGTTCTGCTTTGACAATACATTACAGCACCATT
TCTGAGAAGGTGATTTTCTTTGAATTAATCCTGGATAATATGGGAGAACAGGCACAAGAACAAGAAGATTGGAAG
AAATATATTACTGGCACAGATATATTGGATATGAACTGGAAGACATCCTGGAATCCATCAACAGCATCAAGTCC
AGACTAAGCAAAAGTGGGCACATACAAATCTGCCTTAGAGCATTGGAAGCTCGTGATCGAAACATACAAGAAAGC
AAGTTTGATAGAGTCAATTTCTGGTCTATGGTTAATTTAGTGGTCATGGTGGTGGTGTGTCAGCCATTCAAGTTTAT
ATGCTGAAGAGTCTGTTTGAAGATAAGAGGAAAAAGTAGAAGTTAAACTCCAACTAGAGTACGTAACATTGAAA
AATGAGGCATAAAAAATGCAATAAACTGTTACAGTCAAGACCATTAAATGGTCTTCTCCAAATATTTTGAGATATA
AAAGTAGGAAACAGGTATAATTTAATGTGAAAATTAAGTCTTCACTTTCTGTGCAAGTAATCCTGCTGATCCAG
TTGTACTTAAGTGTGTAACAGGAATATTTTGCAGAATATAGGTTTAACTGAATGAAGCCATATTAATAACTGCAT
TTTCTTAACCTTTGAAAAATTTTGCAAATGTCTTAGGTGATTAAATAAATGAGTATTGGGCCTAATTGCAACACC
AGTCTGTTTTTTAAACAGGTTCTATTACCCAGAACTTTTGTAAATGCGGCAGTTACAAATTAAGTGTGGAAGTTT
TCAGTTTTAAGTTATAAATCACCTGAGAATTACCTAATGATGGATTGAATAAATCTTTAGACTACAAAAGCCCAA
CTTTCTCTATTTACATATGCATCTCTCTATAATGTAAATAGAATAATAGCTTTGAAATACAATTAGGTTTTTG
AGATTTTTTATAACCAAATACATTTCAAGTGAACATATTAGCAGAAAGCATTAGTCTTTGTACTTTGCTTACATTC
CCAAAGCTGACATTTTACGATTCTTAAAAACACAAAGTTACACTTACTAAAATTAGGACATGTTTTCTCTTTG
AAATGAAGAATATAGTTTTAAAGCTTCTCTCCATAGGGACACATTTTCTCTAACCTTAACTAAAGTGTAGGA
TTTTAAAAATTAATGTGAGGTAAATAAGTTTATTTTAAATAGTATCTGTCAAGTTAATATCTGTCAACAGTTAA
TAATCATGTTATGTTAATTTTAAATGATTGCTGACTTGGATAATTCAATTATTACCAGCAGTTATGAAGGAAATA
TTGCTAAAATGATCTGGGCCTACCATAAATAAATATCTCTTTTCTGAGCTCTAAGAATTATCAGAAAACAGGAA
AGAATTTAGAAAACTTGAGAAAACCTAATCCAAATTAATTAAGTGAAGTAAATAAATAATCTAGTA
ATCTGACTGGCTCATCATGACATCCTACTCATAACATAAATCAAAGGAGATGATTAATTTCCAGTTAGCTGGAAG
AACTTTGGCTGTAGGTTTTTATTTTCTACAAGAATTCTGGTTTGAATTATTTTGTAAAGCAGGTACATTTTATA
AAATGTAAGCCCTACTGTAAGGTTTAGCACTGGGTGACATATTTTATTAAAAATTTTATTATAACAACATTTTAT
TAAATGGCCTTTCTGAACACTTTATTTATTGATGTTGAAGTAAGGATTAGAAACATAGACTCCCAAGTTTAAAA
CACCTAAATGTGAATAACCCATATATACAACAAAGTTTCTGCCATCTAGCTTTTGAAGTCTATGGGGGTCTTAC
TCAAGTACTAGTAATTTAACTTCATCATGAATGAAGTATAATTTTAAAGTTATGCCCATTTATAACGTTGTTTAT
GACTACATTGTGAGTTAGAAACAACTTAAATTTGGGGTATAGAACCCCTCAACAGGTTAGTAATGCTGGAATT
CTTGATGAGCAATAATGATAACCAGAGAGTGATTTCACTTACACTCATAGTAGTATAAAAAGAGATACATTTCCC
TCTTAGGCCCCCTGGGAGAAGAGCAGCTTAGATTTCCCTACTGGCAAGGTTTTTAAAAATGAGGTAAATGCCGTAT
ATGATCAATTACCTTAATTGGCCAAGAAAATGCTTCAGGTGTCTAGGGGTATCCTCTGCAACACTTGCAGAACAA
AGGTCAATAAGATCCTTGCCCTATGAATACCCCTCCCTTTTGGCGTGTTAAATTTGCAATGAGAAGCAAAATTTACA
GTACCATAACTAATAAAGCAGGGTACAGATATAAACTACTGCATCTTTTCTATAAACTGTGATTAAGAATTTCTA
CCTCTCCTGTATGGCTGTTACTGTACTGTACTCTCTGACTCCTTACCTAACAATGAATTTGTTACATAATCTTCT
ACATGTATGATTTGTGCCACTGATCTTAAACCTATGATTCAGTAACTTCTTACCATATAAAAACGATAATTGCTT
TATTTGGAAGAAGATTTAGGAATACTAAGGACAATTATTTTTATAGACAAAGTAAAAAGACAGATATTTAAGAGG
CATAACCAAAAAAGCAAACTTGTAACAGAGTAAAAATCTTTAATATTTCTAAAGACATACTGTTTATCTGCTT
CATATGCTTTTTTTAATTTCACTATTCCATTTCTAAATTAAGTTATGCTAAATTGAGTAAGCTGTTTATCACTT
AACAGCTCATTTTGTCTTTTTCAATATACAAATTTTAAAAATACTACAATATTTAACTAAGGCCCAACCGATTTC
CATAATGTAGCAGTTACCGTGTTACCTCACACTAAGGCCCTAGAGTTTGTCTGATATGCATTTGGATGATTAAT
GTTATGCTGTTCTTTTATGTGAATGTCAAGACATGGAGGGTGTGTTGTAATTTTATGGTAAAATTAATCCTTCTTA
CACATAATGGTGTCTTAAATTTGACAAAAATGAGCACTTACAATTTGATGTCTCCTCAAATGAAGATTCTTTAT
GTGAAATTTTAAAGACATTGATTCCGCATGTAAGGATTTTTCATCTGAAGTACAATAATGCACAATCAGTGTTG
CTCAAAGTCTTTTATACTTATAAACAGCCATCTTAAATAAGCAACGTATTGTGAGTACTGATATGTATATAATAA
AAATTATCAAAGGAAAA

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FIGURE 181

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52196

><subunit 1 of 1, 229 aa, 1 stop

><MW: 26017, pI: 4.73, NX(S/T): 0

MGDKIWLPFPVLLLAALPPVLLPGAAGFTPSLDSDFTFITLPAGQKECFYQPMPLKASLEIEY
QVLDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCDNTFSTISEKVIFFEL
ILDNMGEQAQEQEDWKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDRN
IQESNFDRVNFWSMVNLVVMVVVSAIQVYMLKSLFEDKRKSRT

Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 195-217

N-myristoylation site.

amino acids 43-48

Tyrosine kinase phosphorylation site.

amino acids 55-62

09978187.101501

FIGURE 182

CCATCCCTGAGATCTTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATACCAGAT
CTCACCAGAGAGTCGCAGACACTATGCTGCCTCCCATGGCCCTGCCCAGTGTGTCCTGGATG
CTGCTTTCCTGCCTCATTCTCCTGTGTGTCAGGTTCAAGGTGAAGAAACCCAGAAGGAACTGCC
CTCTCCACGGATCAGCTGTCCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGT
TTTTGTACCAAATCCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGGAAAA
CTGGTGTCTGTGCTCAGTGGGGCTGAGGGATCCTTCGTGTCCTCCCTGGTGAGGAGCATTAG
TAACAGCTACTCATACATCTGGATTGGGCTCCATGACCCACACAGGGCTCTGAGCCTGATG
GAGATGGATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAAATCCC
TCCACCATCTTAAACCCTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTG
GAAAGATTATAACTGTGATGCAAAGTTACCCTATGTCTGCAAGTTCAAGGACTAGGGCAGGT
GGGAAGTCAGCAGCCTCAGCTTGGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGAC
TCACCCTGGAAGAGAATATTCTCCCCAACTGCCCTACCTGACTACCTTGTCATGATCCTCC
TTCTTTTTCCTTTTCTTCACCTTCATTTAGGCTTTTCTCTGTCTTCCATGTCTTGAGATC
TCAGAGAATAATAATAAAAATGTTACTTTATAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 183

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965

<subunit 1 of 1, 175 aa, 1 stop

<MW: 19330, pI: 7.25, NX(S/T): 1

MLPPMALPSVSWMLLSCLILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWM
DADLACQKRPSGKLVSVLSGAEGSFVSSLVRSISNSYSYIWIGLHDPTQGSEPDGDGWEWSS
TDVMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPYVCKFKD

Important features:

Signal peptide:

amino acids 1-26

C-type lectin domain signature.

amino acids 146-171

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FIGURE 184

CCAGTCTGTCGCCACCTCACTTGGTGTCTGCTGTCCCCGCCAGGCAAGCCTGGGGTGAGAGC
ACAGAGGAGTGGGCCGGGACCATGCGGGGGACGCGGCTGGCGCTCCTGGCGCTGGTGCTGGC
TGCCTGCGGAGAGCTGGCGCCGGCCCTGCGCTGCTACGTCTGTCCGGAGCCCACAGGAGTGT
CGGACTGTGTCACCATCGCCACCTGCACCACCAACGAAACCATGTGCAAGACCACACTCTAC
TCCCGGGAGATAGTGTACCCCTTCCAGGGGGACTCCACGGTGACCAAGTCCTGTGCCAGCAA
GTGTAAGCCCTCGGATGTGGATGGCATCGGCCAGACCCTGCCCCGTGTCTGTGCAATACTG
AGCTGTGCAATGTAGACGGGGCGCCCGCTCTGAACAGCCTCCACTGCGGGGCCCTCACGCTC
CTCCCACTCTTGAGCCTCCGACTGTAGAGTCCCCGCCCACCCCCATGGCCCTATGCGGCCCA
GCCCCGAATGCCTTGAAGAAGTGCCCCCTGCACCAGGAAAAAAAAAAAAAAAAAAAA

09978187-101501

FIGURE 185

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56405

<subunit 1 of 1, 125 aa, 1 stop

<MW: 13115, pI: 5.90, NX(S/T): 1

MRGTRLALLALVLAACGELAPALRCYVCPEPTGVSDCVTIATCTTNETMCKTTLYSREIVYP
FQGDSTVTKSCASKCKPSDVDGIGQTLFVSCCNTELCNVDGAPALNSLHCGALTLLPLLSLRL

Important features:

Signal peptide:

amino acids 1-17

N-glycosylation site.

amino acids 46-49

09978187.101501

FIGURE 186

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGGACCCTGACTCTGCAGCCGAACCGGC
ACGGTTTTCGTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTCTTTCTTTCTCCCTCTT
GAGTCCTTCTGAGATGATGGCTCTGGGCGCAGCGGGAGCTACCCGGGTCTTTGTGCGGATGG
TAGCGGCGGCTCTCGGCGGCCACCCTCTGCTGGGAGTGAGCGCCACCTTGAACCTCGGTTCTC
AATTCCAACGCTATCAAGAACCTGCCCCACCGCTGGGCGGCGCTGCGGGGCACCCAGGCTC
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA
ACTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT
CCCACCCGCGGAGGGGACGCAGGCGTGCAAATCTGTCTCGCCTGCAGGAAGCGCCGAAAACG
CTGCATGCGTCACGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTCTT
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT
CATAGCACCTTGGATGGGTATTCCAGAAGAACCACCTTGTCTTCAAAAATGTATCACACCAA
AGGACAAGAAGGTTCTGTTTGTCTCCGGTCATCAGACTGTGCCTCAGGATTGTGTTGTGCTA
GACACTTCTGGTCCAAGATCTGTAAACCTGTCTGAAAGAAGGTCAAGTGTGTACCAAGCAT
AGGAGAAAAGGCTCTCATGGACTAGAAATATTCCAGCGTTGTTACTGTGGAGAAGGTCTGTC
TTGCCGGATACAGAAAGATCACCATCAAGCCAGTAATTCTTCTAGGCTTCACACTTGTCAGA
GACACTAAACCAGCTATCCAAATGCAGTGAACTCCTTTTATATAATAGATGCTATGAAAACC
TTTTATGACCTTCATCAACTCAATCCTAAGGATATACAAGTTCTGTGGTTTCAGTTAAGCAT
TCCAATAACACCTTCCAAAAACCTGGAGTGTAAGAGCTTTGTTTCTTTATGGAACCTCCCCTG
TGATTGCAGTAAATTACTGTATTGTAAATTCTCAGTGTGGCACTTACCTGTAAATGCAATGA
AACTTTTAATTATTTTTCTAAAGGTGCTGCACTGCCTATTTTTCTCTTGTATGTAAATTT
TTGTACACATTGATTGTTATCTTGACTGACAAATATTCTATATTGAACTGAAGTAAATCAT
TCAGCTTATAGTTCTTAAAAGCATAACCCTTTACCCCATTTAATTCTAGAGTCTAGAACGCA
AGGATCTCTTGGAATGACAAATGATAGGTACCTAAAATGTAACATGAAAATACTAGCTTATT
TTCTGAAATGTACTATCTTAATGCTTAAATTATATTTCCCTTTAGGCTGTGATAGTTTTTGA
AATAAAATTTAACATTTAAAAAAAAAAAAA

FIGURE 187

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57530

<subunit 1 of 1, 266 aa, 1 stop

<MW: 28672, pI: 8.85, NX(S/T): 1

MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSA
APGILYPGGNKYQTIDNYQPYPCAEDEECGTDEYCASPTRGGDAGVQICLACRKRRCMRH
AMCCPGNYCKNGICVSSDQNHFRGEIEETITESFGNDHSTLDGYSRRTTLSSKMYHTKGQEG
SVCLRSSDCASGLCCARHFWSKICKPVLKEGQVCTKHRRKGSHGLEIFQRCYCGEGLSCRIQ
KDHHQASNSSLHTCQRH

Important features:

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 256-259

Fungal Zn(2)-Cys(6) binuclear cluster domain

amino acids 110-126

FIGURE 188

TGTGTTTCCCTGCAGTCAGAATTTGGGACNGCAGGGGTTCCCGGACCTGATTTTGCAGCGGA
ACGGGAAGGTTTTGTGGGACCCAGGTTGAAATGACGGTCATTTTTTTTTCTTTCTCCTTCNG
GAGTCCTTNTGAGANGATGGTTTTGGGCGCAGCGGGAGCTAACCCGGTTTTTTGTNGCGATG
GTAGCGGCGGTTTTTCGGCGGCCACCTTNTGCTGGGAGTGAGCGCCACCTTGAATCGGTTTTTC
AATTCCAACGNTATCAAGAACCTGCCCCACCGNTGGGCGGCGCTGCGGGGCACCCAGGNTT
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA
ATTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT
CCCACCCGCGGAGGGGANGCGGGCGTGCAAATNTGTNTNGCCTGCAGGAAGCGCCGAAAACG
CTGCATGCGTCANGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTNTT
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT
CATAGCACCTTGGATGGG

09978187.101501

FIGURE 189

GAGGAACCTACCGGTACCGGCCGCGCGCTGGTAGTCGCGCGGTGTGGCTGCACCTCACCAATCCCGTGCGCCGCGG
 CTGGGCCGTCGGAGAGTGCCTGTGCTTCTCTCCTGCACGCGGTGCTTGGGCTCGGCCAGGCGGGGTCCGCCGCCA
 GGGTTTGAGGATGGGGGAGTAGCTACAGGAAGCGACCCCGCGATGGCAAGGTATATTTTGTGGAATGAAAAGGA
 AGTATTAGAAATGAGCTGAAGACCATTACAGATTAAATATTTTGGGGACAGATTTGTGATGCTTGATTACCCCT
 TGAAGTAATGTAGACAGAAGTTCTCAAATTTGCATATTACATCAACTGGAACCAGCAGTGAATCTTAATGTTTAC
 TTAAATCAGAACTTGCATAAGAAAGAGAATGGGAGTCTGGTTAAATAAAGATGACTATATCAGAGACTTGAAAAG
 GATCATTCTCTGTTTTCTGATAGTGTATATGGCCATTTTAGTGGGCACAGATCAGGATTTTTACAGTTTACTTGG
 AGTGTCCAAAACCTGCAAGCAGTAGAGAAAATAAGACAAGCTTTCAAGAAATTGGCATTGAAGTTACATCCTGATAA
 AAACCCGAATAACCCAAATGCACATGGCGATTTTTTAAAAATAAATAGAGCATATGAAGTACTCAAAGATGAAGA
 TCTACGGAAAAAGTATGACAAATATGGAGAAAAAGGACCTTGAGGATAATCAAGGTGGCCAGTATGAAAAGCTGGAA
 CTATTATCGTTATGATTTTTGGTATTTATGATGATGATCCTGAAATCATAACATTGGAAAGAAGAGAATTTGATGC
 TGCTGTTAATTCTGGAGAAGTGTGGTTTGTAAATTTTTACTCCCCAGGCTGTTTCACTGCCATGATTTAGCTCC
 CACATGGAGAGACTTTGCTAAAGAAGTGGATGGGTACTTTCGAATTGGAGCTGTAACTGTGGTGATGATAGAAT
 GCTTTGCCGAATGAAAGGAGTCAACAGCTATCCCAGTCTCTTCATTTTTCGGTCTGGAATGGCCCCAGTGAAATA
 TCATGGAGACAGTCAAAGGAGAGTTTAGTGAGTTTTGCAATGCAGCATGTAGAAAGTACAGTGACAGAACTTTG
 GACAGGAAATTTTGTCAACTCCATACAAACTGCTTTTGCTGCTGGTATTGGCTGGCTGATCACTTTTTGTTCAAA
 AGGAGGAGATTGTTTGACTTTCACAGACACGACTCAGGCTTAGTGGCATGTTGTTTTCTCAACTCATTGGATGCTAA
 AGAAATATATTTGGAAGTAATACATAATCTTCCAGATTTTGAAGTACTTTCCGCAACACACTAGAGGATCGTTT
 GGCTCATCATCGGTGGCTGTTATTTTTTCATTTTGGAAAAAATGAAAATTCAAATGATCCTGAGCTGAAAAAACT
 AAAAAGTCTACTTAAAAATGATCATATTCAAGTTGGCAGGTTTGAAGTCTCTCTGCACCAGACATCTGTAGTAA
 TCTGTATGTTTTTTCAGCCGTCTCTAGCAGTATTTAAAGGACAAGGAACCAAAGAATATGAAATTCATCATGGAAA
 GAAGATTCTATATGATATACTTGCCTTTGCCAAAGAAAGTGTGAATTTCTCATGTTACCACGCTTGGACCTCAAAA
 TTTTCTGCGCAATGACAAAGAACCATGGCTTGTGATTTCTTTGCCCCCTGGTGTCCACCATGTGAGCTTTACT
 ACCAGAGTTACGAAGAGCATCAAATCTTCTTTATGGTCAGCTTAAGTTTGGTACACTAGATTGTACAGTTCATGA
 GGGACTCTGTAACATGTATAACATTACAGGCTTATCCAACAACAGTGGTATTCAACCAGTCCAACATTTCATGAGTA
 TGAAGGACATCACTCTGCTGAACAAATCTTGGAGTTCATAGAGGATCTTATGAATCCTTCAGTGGTCTCCCTTAC
 ACCCACCACCTTCAACGAATGATTACACAAAGAAAACACAACGAAGTCTGGATGGTTGATTTCTATTCTCCGTG
 GTGTCATCCTTGCCAAAGTCTTAATGCCAGAATGGAAAAAGAAATGGCCCGGACATTAACTGGACTGATCAACGTGGG
 CAGTATAGATTGCCAACAGTATCATTCTTTTTGTGCCCGAGGAAAACGTTCAAAGATACCCTGAGATAAGATTTTT
 TCCCCCAAATCAAATAAAGCTTATCAGTATCACAGTTACAATGGTTGGAATAGGGATGCTTATTCCCTGAGAAT
 CTGGGGTCTAGGATTTTTACCTCAAGTATCCACAGATCTAACACCTCAGACTTTTCACTGAAAAAGTTCTACAAGG
 GAAAAATCATTGGGTGATTGATTTCTATGCTCCTTGGTGTGGACCTTGCCAGAATTTTGTCTCCAGAATTTGAGCT
 CTTGGCTAGGATGATTAAAGGAAAAGTGAAAGCTGGAAGTAGACTGTCAGGCTTATGCTCAGACATGCCAGAA
 AGCTGGGATCAGGGCTTATCCAAGTCTTAAGTTTATTTCTAGCTCAGAGCCATACAAAAGTAGGCTGGATTCACTCATG
 GATAAATACCAGAGATGCAAAAGCAATCGCTGCCCTTAATAAGTGAAAAATTGGAAACTCTCCGAAATCAAGGCAA
 GAGGAATAAGGATGAACCTTGATAATGTTGAAGATGAAGAAAAAGTTTAAAGAAATTTCTGACAGATGACATCAG
 AAGACACCTATTTAGAATGTTACATTTATGATGGGAATGAATGAACATTATCTTAGACTTGCAGTTGTACTGCCA
 GAATTATCTACAGCACTGGTGTAAAAGAAGGGTCTGCAAACTTTTTCTGTAAAGGGCCGGTTTATAAATATTTTA
 GACTTTGCAGGCTATAATATATGTTTACACATGAGAACAAGAATAGAGTCATCATGTATTCTTTGTTATTTGCT
 TTTAACAACCTTTAAAAAATATTTAAACGATTCTTAGCTCAGAGCCATACAAAAGTAGGCTGGATTCACTCCATG
 GACCATAGATTGCTGTCCCCCTCGACGGACTTATAATGTTTCAGGTGGCTGGCTTGAACATGAGTCTGCTGTGCT
 ATCTACATAAATGTCTAAGTTGTATAAAGTCCACTTTCCCTTCACGTTTTTTGGCTGACCTGAAAAGAGGTAAC
 TAGTTTTTGGTCACTTGTCTCCTAAAAATGCTATCCCTAACCATATATTTATATTTTCTGTTTTAAAAACACCCAT
 GATGTGGCACAGTAAACAAACCTGTTATGCTGTATTATATGAGGAGATTCTTCATTGTTTTCTTTCTCTCTCA
 AAGGTTGAAAAAATGCTTTTAAATTTTTTACAGCCGAGAAACAGTGCAGCAGTATATGTGCACACAGTAAGTACAC
 AAATTTGAGCAACAGTAAGTGCACAAATCTGTAGTTTGTGTATCATCCAGGAAAACCTGAGGGAAAAAATTA
 TAGCAATTAACGGGCATTGTAGAGTATCCTAAATATGTTATCAAGTATTTAGAGTTCTATATTTTAAAGATATA
 TGTGTTTATGATTTTTCTGAAATTGCTTTTATAGAAAATTTTCCCACTGATAGTTGATTTTTGAGGCATCTAATAT
 TTACATATTTGCCTTCTGAACCTTTGTTTTGACCTGTATCCTTTATTTACATTGGGTTTTTCTTTTATAGTTTGG
 TTTTCTACTCCTGTCCAGTCTATTTATTATTTCAAATAGGAAAAATTACTTTACAGGTTGTTTTACTGTAGCTTAT
 AATGATACTGTAGTTATTTCCAGTTACTAGTTTACTGTGAGAGGGCTGCCTTTTTTTCAGATAAATATTGACATAATA
 ACTGAAGTTATTTTTTAAAGAAATCAAGTATATAAATCTAGGAAAAGGATCTTCTAGTTTTCTGTGTTGTTTGA
 CTCAAAGAATCACAAATTTGTGAGTAACATGTAGTTGTTTGTATATAATTCAGAGTGTACAGAATGGTAAAAAT
 CCAATCAGTCAAAAGAGGTCAATGAATTTAAAGGCTTGCAACTTTTTTCAAAAAAAAAAAAAAAAAA

FIGURE 190

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56439

<subunit 1 of 1, 747 aa, 1 stop

<MW: 86127, pI: 7.46, NX(S/T): 2

MGVWLNKDDYIRD LKRIILCFLIVYMAILVGT DQDFYSL LGVSKTASSREIRQAFKKLALKL
HPDKNPNNPNAHGDF LKINRAYEVLKDEDLRKKYDKYGEK GLEDNQGGQYESWNYRYDFGI
YDDDPEIITLERREFDA AVNSGELW FVNFYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNC
GDDRMLCRMKG VNSYPSLFIFRSGMAPVKYHGDRSKE SLVSFAMQHVRSTVTELWTGNFVNS
IQTAFAAGIGWLITFC SKGGDCLTSQTRLRLSGMLF LNSLDAKEIYLEVIHNLPDFELLSAN
TLEDRLAHRWLLFFHFGKNENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICS NLYVFQP
SLAVFKGQGTKEYEIH HGKKILYDILAFAKESVNSHVTTLGPQNFPANDKEPWLVDFFAPWC
PPCRALLPELRRASN LLYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVVFNQSNIEYEGHHS
AEQILEFIEDLMNP SVVSLTPTTFNELVTQRKHNEVWMVDFYSPWCHPCQVLMPEWKRMART
LTGLINVGSIDCQQYHSFCAQENVQRYPEIRFFPPKSNKAYQYHSYNGWNRDAYSLRIWGLG
FLPQVSTD LTPQTFSEKVLQGNHWVIDFYAPWCGPCQNFAP EPELLARMIKGKVKAGKVDC
QAYAQTCQKAGIRAYPTVKFYFYERAKRNFQEEQINTRDAKAIAALISEKLETLRNQGKRNKDEL

Important features:

Endoplasmic reticulum targeting sequence.

amino acids 744-747

Cytochrome c family heme-binding site signature.

amino acids 158-163

Nt-dnaJ domain signature.

amino acids 77-96

N-glycosylation site.

amino acids 484-487

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TOSTOT 282660

FIGURE 191

AGACAGTACCTCCTCCCTAGGACTACACAAGGACTGAACCAGAAGGAAGAGGACAGAGCAAA
GCCATGAACATCATCCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCCTACTTGGA
GTCGTTGGTGAAGTTTTTCATTCCCTCAGAGGAGAAAATCTGTGGCTGGGGAGATTGTTCTCA
TTACTGGAGCTGGGCATGGAATAGGCAGGCAGACTACTTATGAATTTGCAAAACGACAGAGC
ATATTGGTTCTGTGGGATATTAATAAGCGCGGTGTGGAGGAACTGCAGCTGAGTGCCGAAA
ACTAGGCGTCACTGCGCATGCGTATGTGGTAGACTGCAGCAACAGAGAAGAGATCTATCGCT
CTCTAAATCAGGTGAAGAAAGAAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACA
GTATATCCAGCCGATCTTCTCAGCACCAAGGATGAAGAGATTACCAAGACATTTGAGGTCAA
CATCCTAGGACATTTTTTGGATCACAAAAGCACTTCTTCCATCGATGATGGAGAGAAATCATG
GCCACATCGTCACAGTGGCTTCAGTGTGCGGCCACGAAGGGATTCCCTACCTCATCCCATAT
TGTTCCAGCAAATTTGCCGCTGTTGGCTTTCACAGAGGTCTGACATCAGAACTTCAGGCCTT
GGGAAAACTGGTATCAAAACCTCATGTCTCTGCCAGTTTTTGTGAATACTGGGTTCACCA
AAAATCCAAGCACAAAGATTATGGCCTGTATTGGAGACAGATGAAGTCGTAAGAAGTCTGATA
GATGGAATACTTACCAATAAGAAAATGATTTTTTGTTCATCGTATATCAATATCTTTCTGAG
ACTACAGAAGTTTCTTCCTGAACGCGCCTCAGCGATTTTAAATCGTATGCAGAATATTCAAT
TTGAAGCAGTGGTTGGCCACAAAATCAAAATGAAATGGAATAAATAAGCTCCAGCCAGAGATG
TATGCATGATAATGATATGAATAGTTTCGAATCAATGCTGCAAAGCTTTATTTTCACATTTTT
TCAGTCCTGATAATATTA AAAACATTGGTTTGGCACTAGCAGCAGTCAAACGAACAAGATTA
ATTACCTGTCTTCCTGTTTCTCAAGAATATTTACGTAGTTTTTTCATAGGTCTGTTTTTCCTT
TCATGCCTCTTAAAACTTCTGTGCTTACATAAACATACTTAAAAGGTTTTCTTTAAGATAT
TTTATTTTTTCCATTTAAAGGTGGACAAAAGCTACCTCCCTAAAAGTAAATACAAAGAGA
TATTTACACAGGGAAGGTTTAAGACTGTTCAAGTAGCATTCCAATCTGTAGCCATGCCACAG
AATATCAACAAGAACACAGAATGAGTGCACAGCTAAGAGATCAAGTTTCAGCAGGCAGCTTT
ATCTCAACCTGGACATATTTTAAGATTGAGCATTTGAAAGATTTCCCTAGCCTCTTCCTTTT
TCATTAGCCCAAAACGGTGCAACTCTATTCTGGACTTTATTACTTGATTCTGTCTTCTGTAT
AACTCTGAAGTCCACCAAAAGTGGACCCTCTATATTTCCCTCCCTTTTTATAGTCTTATAAGA
TACATTATGAAAGGTGACCGACTCTATTTTAAATCTCAGAATTTTAAGTTCTAGCCCCATGA
TAACCTTTTTCTTTGTAATTTATGCTTTCATATATCCTTGGTCCCAGAGATGTTTAGACAAT
TTTAGGCTCAAAAATTAAAGCTAACACAGGAAAAGGAACTGTACTGGCTATTACATAAGAAA
CAATGGACCCAAGAGAAGAA

FIGURE 192

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409

<subunit 1 of 1, 300 aa, 1 stop

<MW: 33655, pI: 9.31, NX(S/T): 1

MNIILEILLLLITIIYSYLESLVKFFIPQRRKSVAGEIVLITGAGHGIGRQTTYEFAKRQSI
LVLWDINKRGVEETAAECKRLGVTAHAYVVDCSNREEIYRSLNQVKKEVGDTVIVVNNAGTV
YPADLLSTKDEEITKTFEVNILGHFWITKALLPSMMERNHGHIVTVASVCGHEGIPYLIPYC
SSKFAAVGFHRGLTSELQALGKTGIKTSCLCPVFNVTGFTKNPSTRLWPVLETDEVVRSLID
GILTNNKKMIFVPSYINIFLRLQKFLPERASAILNRMQNIQFEAVVGHKIKMK

Important features:

Signal peptide:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-33 and 58-61

Short-chain alcohol dehydrogenase family protein

amino acids 165-202, 37-49, 112-122 and 210-219

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FOSTOT-28782660

FIGURE 193

CGGCGGCGGCTGCGGGCGCGAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGTTCCCAGCAGG
ATGCCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGCCCGGAGAGGGCCCAGCCCCGCGGGGC
AGGATGACCAAGGCCCGGCTGTTCCGGCTGTGGCTGGTGCTGGGGTTCGGTGTTTCATGATCCT
GCTGATCATCGTGTACTGGGACAGCGCAGGCGCCGCGCACTTCTACTTGACACAGTCCTTCT
CTAGGCCGCACACGGGGCCGCGCTGCCACGCCCCGGGCCGACAGGGACAGGGAGCTCACG
GCCGACTCCGATGTGACGAGTTTCTGGACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGA
CCTTCCCAGAAAGGAGACGGAGCAGCCGCCTGCGCCGGGGAGCATGGAGGAGAGCGTGAGAG
GCTACGACTGGTCCCCGCGCGACGCCCCGGCGCAGCCCAGACCAGGGCCGGCAGCAGGCGGAG
CGGAGGAGCGTGCTGCGGGGCTTCTGCGCCAACTCCAGCCTGGCCTTCCCCACCAAGGAGCG
CGCATTTCGACGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGACGACCGGCACGGGG
CCATCTACTGCTACGTGCCCAAGGTGGCCTGCACCAACTGGAAGCGCGTGATGATCGTGCTG
AGCGGAAGCCTGCTGCACCGCGGTGCGCCCTACCGCGACCCGCTGCGCATCCCGCGCGAGCA
CGTGACAACGCCAGCGCGCACCTGACCTTCAACAAGTTCTGGCGCCGCTACGGGAAGCTCT
CCCGCCACCTCATGAAGGTCAAGCTCAAGAAGTACACCAAGTTCCTCTTCGTGCGCGACCCC
TTCGTGCGCCTGATCTCCGCCTTCCGCAGCAAGTTCGAGCTGGAGAACGAGGAGTTCTACCG
CAAGTTCGCCGTGCCCATGCTGCGGCTGTACGCCAACCACACCAGCCTGCCCCGCTCGGCGC
GCGAGGCCTTCCGCGCTGGCCTCAAGGTGTCCTTCGCCAACTTCATCCAGTACCTGCTGGAC
CCGCACACGGAGAAGCTGGCGCCCTTCAACGAGCACTGGCGGCAGGTGTACCGCCTCTGCCA
CCCGTGCCAGATCGACTACGACTTCGTGGGGAAGCTGGAGACTCTGGACGAGGACGCCGCGC
AGCTGCTGCAGCTACTCCAGGTGGACCGGCAGCTCCGCTTCCCCCGAGCTACCGGAACAGG
ACCGCCAGCAGCTGGGAGGAGGACTGGTTCGCCAAGATCCCCCTGGCCTGGAGGCAGCAGCT
GTATAAACTCTACGAGGCCGACTTTGTTCTCTTCGGCTACCCCAAGCCCGAAAACCTCCTCC
GAGACTGAAGCTTTCGCGTTGCTTTTTCTCGCGTGCTTGGAACTGACGCACGCGCACTCC
AGTTTTTTTATGACCTACGATTTTGCAATCTGGGCTTCTTGTTCACTCCACTGCCTCTATCC
ATTGAGTACTGTATCGATATTGTTTTTTAAGATTAATATATTTTCAGGTATTTAATACGA

FIGURE 194

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56112

<subunit 1 of 1, 414 aa, 1 stop

<MW: 48414, pI: 9.54, NX(S/T): 4

MTKARLFRLWLVLGSVFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPPLPTPGPDRDRELT
DSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRGYDWSPRDARRSPDQGRQQAER
RSVLRGFCANSSLAFTKERAFFDDIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLS
GSLLRGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKLKKYTKFLFVRDPF
VRLISAFRSKFELENEEFYRKFAVPMLRLYANHTSLPASAREAFRAGLKVSFANFIQYLLDP
HTEKLAPFNEHWRQVYRLCHPCQIDYDFVGKLETLDDEAAQLLQLLQVDRQLRFPPSYRNRT
ASSWEEDWFAKIPLAWRQQLYKLYEADFVLFGYPKPENLLRD

Important features:

Signal peptide:

amino acids 1-31

N-glycosylation sites.

amino acids 134-137, 209-212, 280-283 and 370-373

TNFR/NGFR family cysteine-rich region protein

amino acids 329-332

FIGURE 195

TCGGGCCAGAATTCGGCACGAGGCGGCACGAGGGCGACGGCCTCACGGGGCTTTGGAGGTGA
AAGAGGCCCCAGAGTAGAGAGAGAGAGAGACCGACGTACACGGGATGGCTACGGGAACGCGCT
ATGCCGGGAAGGTGGTGGTCGTGACCGGGGGCGGGCGCGGCATCGGAGCTGGGATCGTGCGC
GCCTTCGTGAACAGCGGGGGCCCGAGTGGTTATCTGCGACAAGGATGAGTCTGGGGGCCGGGC
CCTGGAGCAGGAGCTCCCTGGAGCTGTCTTTATCCTCTGTGATGTGACTCAGGAAGATGATG
TGAAGACCCTGGTTTCTGAGACCATCCGCCGATTTGGCCGCCTGGATTGTGTTGTCAACAAC
GCTGGCCACCACCCACCCCCACAGAGGCCTGAGGAGACCTCTGCCCAGGGATTCCGCCAGCT
GCTGGAGCTGAACCTACTGGGGACGTACACCTTGACCAAGCTCGCCCTCCCCTACCTGCGGA
AGAGTCAAGGGAATGTCATCAACATCTCCAGCCTGGTGGGGGCAATCGGCCAGGCCCAGGCA
GTTCCCTATGTGGCCACCAAGGGGGCAGTAACAGCCATGACCAAAGCTTTGGCCCTGGATGA
AAGTCCATATGGTGTCCGAGTCAACTGTATCTCCCCAGGAAACATCTGGACCCCGCTGTGGG
AGGAGCTGGCAGCCTTAATGCCAGACCCTAGGGCCACAATCCGAGAGGGCATGCTGGCCCAG
CCACTGGGCCCGCATGGGCCAGCCCGCTGAGGTGCGGGCTGCGGCAGTGTTCTTGGCCTCCGA
AGCCAACTTCTGCACGGGCATTGAACTGCTCGTGACGGGGGGTGCGAGAGCTGGGGTACGGGT
GCAAGGCCAGTCGGAGCACCCCCGTGGACGCCCCCGATATCCCTTCCTGATTTTCTCTCATTT
CTACTTGGGGCCCCCTTCCTAGGACTCTCCACCCCAAACCTCCAACCTGTATCAGATGCAGC
CCCCAAGCCCTTAGACTCTAAGCCCAGTTAGCAAGGTGCCGGGTACCCTGCAGGTTCCCAT
AAAAACGATTTGCAGCC

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FIGURE 196

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56045

<subunit 1 of 1, 270 aa, 1 stop

<MW: 28317, pI: 6.00, NX(S/T): 1

MATGTRYAGKVVVVVTGGGRGIGAGIVRAFVNSGARVVICDKDESGGRALEQELPGAVFILCD
VTQEDDVKTLVSETIRRFGRLCDVNNAGHHPPPQRPEETSAQGFRQLLELNLLGTYTLTKL
ALPYLRKSQGNVINISLVGAIGQAQAVPYVATKGAVTAMTKALALDESPYGVRVNCISPGN
IWTPLWEELAALMPDPRATIREGMLAQPLGRMGQPAEVGAAAVFLASEANFCTGIELLVTTGG
AELGYGCKASRSTPVDAPDIPS

Important features:

N-glycosylation site.

amino acids 138-141

Short-chain alcohol dehydrogenase family protein

amino acids 10-22, 81-91, 134-171 and 176-185

09978187.101501
FOSTOT.28282660

FIGURE 197

AGGCGGGCAGCAGCTGCAGGCTGACCTTGCAGCTTGGCGGAATGGACTGGCCTCACAACTG
CTGTTTCTTCTTACCATTTCCATCTTCCTGGGGCTGGGCCAGCCCAGGAGCCCCAAAAGCAA
GAGGAAGGGGCAAGGGCGGCCTGGGCCCCCTGGCCCCCTGGCCCTCACCAGGTGCCACTGGACC
TGGTGTACGGATGAAACCGTATGCCCCGATGGAGGAGTATGAGAGGAACATCGAGGAGATG
GTGGCCCAGCTGAGGAACAGCTCAGAGCTGGCCCAGAGAAAGTGTGAGGTCAACTTGCAGCT
GTGGATGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCCAGCC
GTATCCCCGTGGACCTGCCGGAGGCACGGTGCCTGTGTCTGGGCTGTGTGAACCCCTTCACC
ATGCAGGAGGACCGCAGCATGGTGAGCGTGCCGGTGTTTCAGCCAGGTTCCCTGTGCGCCGCCG
CCTCTGCCCCGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCG
CTGTGGGCTGCACCTGCATCTTCTGAATCACCTGGCCCAGAAGCCAGGCCAGCAGCCCGAGA
CCATCCTCCTTGCACCTTTGTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAA
GCAAG

FIGURE 198

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59294

<subunit 1 of 1, 180 aa, 1 stop

<MW: 20437, pI: 9.58, NX(S/T): 1

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRPGPLAPGPHQVPLDLVSRMKPYARMEEY
ERNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPRIIPVDLPEARCLCL
GCVNPFTMQEDRSMVSVPVFSQVPVRRRLCPPPPRTGPCRQRAVMETIavgctcIF

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 75-78

Homologous region to IL-17

amino acids 96-180.

09978187 101501
TOSTOT 28782660

FIGURE 199

GCGCCGCCAGGCGTAGGCGGGGTGGCCCTTGCGTCTCCCGCTTCCTTGAAAAACCCGGCGGG
CGAGCGAGGCTGCGGGCCCGGCCGCTGCCCTTCCCCACACTCCCCGCCGAGAAGCCTCGCTCG
GCGCCCAACATGGCGGGTGGGCGCTGCGGCCCGCAGCTAACGGCGCTCCTGGCCGCCTGGAT
CGCGGCTGTGGCGGCGACGGCAGGCCCGAGGAGGCCGCGCTGCCGCCGAGCAGAGCCGGG
TCCAGCCCATGACCGCCTCCAACCTGGACGCTGGTGATGGAGGGCGAGTGGATGCTGAAATTT
TACGCCCCATGGTGTCCATCCTGCCAGCAGACTGATTTCAGAATGGGAGGCTTTTGCAAAGAA
TGGTGAAATACTTCAGATCAGTGTGGGGAAGGTAGATGTCATTCAAGAACCAGGTTTGAGTG
GCCGCTTCTTTGTCACTACTCTCCAGCATTTTTTTCATGCAAAGGATGGGATATTCCGCCGT
TATCGTGGCCAGGAATCTTCGAAGACCTGCAGAATTATATCTTAGAGAAGAAATGGCAATC
AGTCGAGCCTCTGACTGGCTGGAAATCCCCAGCTTCTCTAACGATGTCTGGAATGGCTGGTC
TTTTTAGCATCTCTGGCAAGATATGGCATCTTCACAACATTTTCACAGTGAATCTTGGAATT
CCTGCTTGGTGTCTTATGTGTTTTTCGTCATAGCCACCTTGGTTTTTGGCCTTTTTTATGGG
TCTGGTCTTGGTGGTAATATCAGAATGTTTCTATGTGCCACTTCCAAGGCATTTATCTGAGC
GTTCTGAGCAGAATCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGCAGGATGCGGAG
GAGGAAAAAGATGATTCAAATGAAGAAGAAAACAAAGACAGCCTTGTAGATGATGAAGAAGA
GAAAGAAGATCTTGGCGATGAGGATGAAGCAGAGGAAGAAGAGGAGGAGGACAACTTGGCTG
CTGGTGTGGATGAGGAGAGAAGTGAGGCCAATGATCAGGGGCCCCCAGGAGAGGACGGTGTG
ACCCGGGAGGAAGTAGAGCCTGAGGAGGCTGAAGAAGGCATCTCTGAGCAACCCTGCCCAGC
TGACACAGAGGTGGTGGAAAGACTCCTTGAGGCAGCGTAAAAGTCAGCATGCTGACAAGGGAC
TGTAGATTTAATGATGCGTTTTCAAGAATACACACCAAAACAATATGTCAGCTTCCCTTTGG
CCTGCAGTTTGTACCAAATCCTTAATTTTTTCTGAATGAGCAAGCTTCTCTTAAAGATGCT
CTCTAGTCATTTGGTCTCATGGCAGTAAGCCTCATGTATACTAAGGAGAGTCTTCCAGGTGT
GACAATCAGGATATAGAAAAACAAACGTAGTGTGGGATCTGTTTGGAGACTGGGATGGGAA
CAAGTTCATTTACTTAGGGGTGAGAGAGTCTCGACCAGAGGAGGCCATTCCCAGTCCTAATC
AGCACCTTCCAGAGACAAGGCTGCAGGCCCTGTGAAATGAAAGCCAAGCAGGAGCCTTGGCT
CCTGAGCATCCCCAAAGTGTAACGTAGAAGCCTTGTCATCCTTTTCTTGTGTAAAGTATTTAT
TTTTGTCAAATTGCAGGAAACATCAGGCACCACAGTGCATGAAAAATCTTTCACAGCTAGAA
ATTGAAAGGGCCTTGGGTATAGAGAGCAGCTCAGAAGTCATCCCAGCCCTCTGAATCTCCTG
TGCTATGTTTTATTTCTTACCTTTAATTTTTTCCAGCATTTCCACCATGGGCATTCAGGCTCT
CCACACTCTTCACTATTATCTCTTGGTGCAGAGGACTCCAATAACAGCCAGGTTTACATGAAC
TGTGTTTGTTCATTCTGACCTAAGGGGTTTAGATAATCAGTAACCATAACCCCTGAAGCTGT
GACTGCCAAACATCTCAAATGAAATGTTGTGGCCATCAGAGACTCAAAGGAAGTAAGGATT
TTACAAGACAGATTAAAAAAAATTTGTTTTGTCCAAAATATAGTTGTTGTTGATTTTTTTTT
AAGTTTTCTAAGCAATATTTTTCAAGCCAGAAGTCCTCTAAGTCTTGCCAGTACAAGGTAGT
CTTGTGAAGAAAAGTTGAATACTGTTTTGTTTTTCATCTCAAGGGGTTCCCTGGGTCTTGAAC
TACTTTAATAATAACTAAAAAACCACTTCTGATTTTCTTTCAGTGATGTGCTTTTGGTGAAA
GAATTAATGAACTCCAGTACCTGAAAGTGAAAGATTTGATTTTGTTCATCTTCTGTAATC
TTCCAAAGAATTATATCTTTGTAAATCTCTCAATACTCAATCTACTGTAAGTACCCAGGGAG
GCTAATTTCTTT

FIGURE 200

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56433

<subunit 1 of 1, 349 aa, 1 stop

<MW: 38952, pI: 4.34, NX(S/T): 1

MAGGRCGPQLTALLAAWIAAVAATAGPEEAALPPEQSRVQPMTASNWTLVMEGEWMLKFYAP
WCPSCQQTDSEWEAFKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGI FRRYRG
PGIFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFSISGKIWHLHNYFTVTLGIPAW
CSYVFFVIATLVFGLFMGLVLVVISSECFYVPLPRHLSE RSEQNRRSEEAHRAEQLQDAEEEEK
DDSNEEENKDSLVDDEEEKEDLGDEDEAE EEEEEEDNLAAGVDEERSEANDQGPPGEDGV TRE
EVEPEEAEGISEQPCPADTEVVEDSLRQRKSQHADKGL

Important features:

Signal peptide:

amino acids 1-22

Transmembrane domain:

amino acids 191-211

N-glycosylation site.

amino acids 46-49

Thioredoxin family proteins. (homologous region to disulfide isomerase)

amino acids 56-72

Flavodoxin proteins

amino acids 173-187

09978187-101501
TOSTOT-2872660

FIGURE 201

ATCTGGTTGAACTACTTAAGCTTAATTTGTTAAACTCCGGTAAGTACCTAGCCCACATGATT
TGACTCAGAGATTCTCTTTTGTCCACAGACAGTCATCTCAGGGGCAGAAAGAAAAGAGCTCC
CAAATGCTATATCTATTTCAGGGGCTCTCAAGAACAATGGAATATCATCCTGATTTAGAAAAT
TTGGATGAAGATGGATATACTCAATTACACTTCGACTCTCAAAGCAATACCAGGATAGCTGT
TGTTTCAGAGAAAGGATCGTGTGCTGCATCTCCTCCTTGGCGCCTCATTGCTGTAATTTTGG
GAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCCTGGGTACCATGGGGGTTCTTTCC
AGCCCTTGTCTCTCCTAATTGGATTATATATGAGAAGAGCTGTTATCTATTTCAGCATGTCACT
AAATTCCTGGGATGGAAGTAAAAGACAATGCTGGCAACTGGGCTCTAATCTCCTAAAGATAG
ACAGCTCAAATGAATTGGGATTTATAGTAAAACAAGTGTCTTCCCAACCTGATAATTCATTT
TGGATAGGCCTTTCTCGGCCCCAGACTGAGGTACCATGGCTCTGGGAGGATGGATCAACATT
CTCTTCTAACTTATTTTCAGATCAGAACCACAGCTACCCAAGAAAACCCATCTCCAAATTGTG
TATGGATTCACGTGTCAGTCATTTATGACCAACTGTGTAGTGTGCCCTCATATAGTATTTGT
GAGAAGAAGTTTTCAATGTAAGAGGAAGGGTGGAGAAGGAGAGAGAAAATATGTGAGGTAGTA
AGGAGGACAGAAAACAGAACAGAAAAGAGTAACAGCTGAGGTCAAGATAAATGCAGAAAATG
TTTAGAGAGCTTGGCCAACCTGTAATCTTAACCAAGAAATTGAAGGGAGAGGCTGTGATTTCT
GTATTTGTGACCTACAGGTAGGCTAGTATTATTTTTCTAGTTAGTAGATCCCTAGACATGG
AATCAGGGCAGCCAAGCTTGAGTTTTTATTTTTTATTTATTTTATTTTTTTGAGATAGGGTCT
CACTTTGTTACCCAGGCTGGAGTGCAGTGGCACAATCTCGACTCACTGCAGCTATCTCTCGC
CTCAGCCCCTCAAGTAGCTGGGACTACAGGTGCATGCCACCATGCCAGGCTAATTTTTTGGTG
TTTTTTGTAGAGACTGGGTTTTGCCATGTTGACCAAGCTGGTCTCTAACTCCTGGGCTTAAG
TGATCTGCCCCGCTTGGCCTCCCAAAGTGCTGGGATTACAGATGTGAGCCACCACACCTGGC
CCCAAGCTTGAATTTTCATTCTGCCATTGACTTGGCATTACCTTGGGTAAGCCATAAGCGA
ATCTTAATTTCTGGCTCTATCAGAGTTGTTTCATGCTCAACAATGCCATTGAAGTGCACGGT
GTGTTGCCACGATTTGACCCTCAACTTCTAGCAGTATATCAGTTATGAACTGAGGGTGAAAT
ATATTTCTGAATAGCTAAATGAAGAAATGGGAAAAAATCTTCACCACAGTCAGAGCAATTTT
ATTATTTTCATCAGTATGATCATAATTATGATTATCATCTTAGTAAAAAGCAGGAACTCCTA
CTTTTTCTTTATCAATTAAATAGCTCAGAGAGTACATCTGCCATATCTCTAATAGAATCTTT
TTTTTTTTTTTTTTTTTTTTTGGAGACAGAGTTTCGCTCTTGTTGCCCAGGCTGGAGTGCAACGG
CACGATCTCGGCTCACCGCAACCTCCGCCCCCTGGGTTCAAGCAATTCTCCTGCCTCAGCCT
CCCAAGTAGCTGGGATTACAGTCAGGCACCACCACACCCGGCTAATTTTTGTATTTTTTTAGT
AGAGACAGGGTTTCTCCATGTCGGTCAGGGTAGTCCCGAACTCCTGACCTCAAGTGATCTGC
CTGCCTCGGCCTCCCAAGTGCTGGGATTACAGGCGTGAGCCACTGCACCCAGCCTAGAATCT
TGTATAATATGTAATTGTAGGGAACTGCTCTCATAGGAAAGTTTTCTGCTTTTTTAAATACA
AAAATACATAAAAAATACATAAAATCTGATGATGAATATAAAAAAGTAACCAACCTCATTGGA
ACAAGTATTAACATTTTGGAAATATGTTTTATTAGTTTTGTGATGTACTGTTTTACAATTTTT
ACCATTTTTTTTCAGTAATTACTGTAAAATGGTATTATTGGAATGAACTATATTTCTCATG
TGCTGATTTGTCTTATTTTTTTTACATACTTTCCCACTGGTGCTATTTTTATTTCCAATGGATA
TTTCTGTATTACTAGGGAGGCATTTACAGTCCTCTAATGTTGATTAATATGTGAAAAGAAAT
TGTACCAATTTTACTAAATTATGCAGTTTAAAATGGATGATTTTATGTTATGTGGATTTTCAT
TTCAATAAAAAAAACTCTTATCAAAAAA

FIGURE 202

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53912

<subunit 1 of 1, 201 aa, 1 stop

<MW: 22563, pI: 4.87, NX(S/T): 1

MEYHPDLENLDEDGYTQLHFDSQSNTRIAVVSEKGS CAASPPWRLIAVILGILCLVILVIAV
VLGTMGVLSSPCPPNWIIYEKSCYLFSMSLNSWDGSKRQCWQLGSNLLKIDSSNELGFIVKQ
VSSQPDNSFWIGLSRPQTVEPWLWEDGSTFSSNLFQIRTTATQENPSPNCVWIHVSVIYDQL
CSVPSYSICEKKFSM

Important features:

Type II transmembrane domain:

amino acids 45-65

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 197-200

N-myristoylation sites.

amino acids 35-40 and 151-156

Homologous region to LDL receptor

amino acids 34-67 and 70-200.

09978187-101501

FIGURE 203

GGAAGGGGAGGAGCAGGCCACACAGGCACAGGCCGGTGAGGGACCTGCCCAGACCTGGAGGGTCTCGCTCTGTCA
 CACAGGCTGGAGTGCAGTGGTGTGATCTTGGCTCATCGTAACCTCCACCTCCCGGGTTCAAGTGATTCTCATGCC
 TCAGCCTCCCGAGTAGCTGGGATTACAGGTGGTGACTTCCAAGAGTGACTCCGTCCGGAGGAAAATGACTCCCCAG
 TCGCTGCTGCAGACGACACTGTTCTCTGCTGAGTCTGCTCTTCTGGTCCAAGGTGCCACGGCAGGGGCCACAGG
 GAAGACTTTTCGCTTCTGCAGCCAGCGGAACCAGACACACAGGAGCAGCCTCCACTACAAACCCACACCAGACCTG
 CGCATCTCCATCGAGAACTCCGAAGAGGCCCTCACAGTCCATGCCCCCTTCCCTGCAGCCCACCCTGCTTCCCGA
 TCCTTCCCTGACCCAGGGGCCCTTACCACCTTCTGCCTCTACTGGAACCGACATGCTGGGAGATTACATCTTCTC
 TATGGCAAGCGTGACTTCTTGTGAGTGACAAAGCCTCTAGCCTCCTCTGCTTCCAGCACCAGGAGGAGAGCCTG
 GCTCAGGGCCCCCGCTGTTAGCCACTTCTGTACCTCTGCTGGTGGAGCCCTCAGAACATCAGCCTGCCAGTGCC
 GCCAGCTTACCTTCTCCTTCCACAGTCTCTCCCCACAGGCCGCTCACAATGCCTCGGTGGACATGTGCGAGCTC
 AAAAGGGACCTCCAGCTGCTCAGCCAGTTCCTGAAGCATCCCCAGAAGGCCTCAAGGAGGCCCTCGGCTGCCCCC
 GCCAGCCAGCAGTTGCAGAGCCTGGAGTCGAAACTGACCTCTGTGAGATTTCATGGGGACATGGTGTCTTTCGAG
 GAGGACCGGATCAACGCCACGGTGTGGAAGCTCCAGCCACAGCCGGCCTCCAGGACCTGCACATCCACTCCCGG
 CAGGAGGAGGAGCAGAGCGAGATCATGGAGTACTCGGTGCTGCTGCCTCGAACACTCTTCCAGAGGACGAAAGGC
 CGGAGCGGGGAGGCTGAGAAGAGACTCCTCCTGGTGGACTTCAGCAGCCAAGCCCTGTTCCAGGACAAGAATTCC
 AGCCAAGTCTGGGTGAGAAGGTCTTGGGGATTGTGGTACAGAACACCAAAGTAGCCAACCTCAGGGAGCCCGTG
 GTGCTCACTTTCAGCACCAGCTACAGCCGAAGAATGTGACTCTGCAATGTGTGTTCTGGGTTGAAGACCCCA
 TTGAGCAGCCCCGGGCATTGGAGCAGTGTGGGTGTGAGACCGTCAGGAGAGAAACCAAACATCCTGCTTCTGC
 AACCATTGACCTACTTTGCAGTGTGATGGTCTCCTCGGTGGAGGTGGACGCCGTGCACAAAGCACTACCTGAGC
 CTCCTCTCCTACGTGGGCTGTGTCTCTGCCCCTGGCCTGCCTTGTCAACATTGCCGCCTACCTCTGCTCCAGG
 GTGCCCCCTGCCGTGCAGGAGGAAACCTCGGACTACACCATCAAGGTGCACATGAACCTGCTGCTGGCCGTCTTC
 GCTTGGACACGAGCTTCTGCTCAGCGAGCCGGTGGCCCTGACAGGCTCTGAGGCTGGCTGCCGAGCCAGTGCC
 ATCTTCTGCACTTCTCCCTGCTCACCTGCCTTTCTGGATGGGCCTCGAGGGGTACAACCTCTACCGACTCGTG
 GTGGAGGTCTTTGGACCTATGTCCCTGGCTACCTACTCAAGCTGAGCGCCATGGGCTGGGGCTTCCCCATCTTT
 CTGGTGACGCTGGTGGCCCTGGTGGATGTGGACAACATATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAG
 GGCCTCATCTACCCTTCCATGTGCTGGATCCGGGACTCCTGGTCAGCTACATCACCAACCTGGGCCTCTTCAGC
 CTGGTGTCTTCTGTTCAACATGGCCATGTAGCCACCATGGTGGTGCAGATCCTGCGGCTGCGCCCCACACCCAA
 AAGTGGTCACATGTGCTGACACTGCTGGGCCCTCAGCCTGGTCTTGGCCTGCCCTGGGCCCTTGATCTTCTTCTCC
 TTTGCTTCTGGCACCTTCCAGCTTGTGCTCTCTACCTTTTCAGCATCATCACTCCTTCCAAGGCTTCTCTATC
 TTCATCTGGTACTGGTCCATGCGGCTGCAGGCCCGGGGTGGCCCCCTCCCCTCTGAAGAGCAACTCAGACAGCGCC
 AGGCTCCCCATCAGCTCGGGCAGCACCTCCTCCAGCCGCATCTAGGCCTCCAGCCCACCTGCCCATGTGATGAAG
 CAGAGATGCGGCCTCGTCGCACACTGCCTGTGGCCCCCGAGCCAGGCCCAGCCCCAGGCCAGTCAGCCGCAGACT
 TTGGAAGCCCAACGACCATGGAGAGATGGGCCGTGGCATGGTGGACGGAATCCCGGGCTGGGCTTTTGAATTG
 GCCTTGGGGACTACTCGGCTCTCACTCAGCTCCACAGGGACTCAGAAGTGCGCCGCCATGCTGCCCTAGGGTACTG
 TCCCCACATCTGTCCCAACCCAGCTGGAGGCCCTGGTCTCTCCTTACAACCCCTGGGCCCAGCCCTCATTTGCTGGG
 GGCCAGGCCTTGGATCTTGAGGGTCTGGCACATCCTTAATCCTGTGCCCTGCCTGGGACAGAAATGTGGCTCCA
 GTTGCTCTGTCTCTCGTGGTCACCTGAGGGCACTCTGCATCCTCTGTCAATTTAACCTCAGGTGGCACCCAGGG
 CGAATGGGGCCCAGGGCAGACCTTCAGGGCCAGAGCCTGGCGGAGGAGAGGCCCTTTGCCAGGAGCACAGCAGC
 AGCTCGCCTACCTCTGAGCCCAGGCCCTCCTCCTCAGCCCCCAGTCTCCTCCTCCATCTTCCCTGGGGTTCT
 TCCTCCTCTCCAGGGCCTCCTTGTCTTCTCGTTACAGCTGGGGGTCCCCGATTCCAATGCTGTTTTTTGGGGA
 GTGGTTTCCAGGAGCTGCCTGGTGTCTGCTGTAAATGTTTGTCTACTGCACAAGCCTCGGCCTGCCCTGAGCCA
 GGCTCGGTACCGATGCGTGGGCTGGGCTAGGTCCCTCTGTCCATCTGGGCCTTTGTATGAGCTGCATTGCCCTTG
 CTCACCCTGACCAAGCACAGCCTCAGAGGGGCCCTCAGCCTCTCCTGAAGCCCTCTTGTGGCAAGAATGTGGA
 CCATGCCAGTCCCGTCTGGTTTCCATCCCAACCTCCAAGGACTGAGACTGACCTCCTCTGGTGACACTGGCCTA
 GAGCCTGACACTCTCCTAAGAGGTCTCTCCAAGCCCCAAATAGCTCCAGGCGCCCTCGGCCGCCCATCATGGT
 TAATTCTGTCCAACAAACACACAGGGTAGATTGTGGCCTGTTGTAGGTGGTAGGGACACAGATGACCGACCTG
 GTCACCTCCTGCCAACATTCACTGTGGTATGTGAGGCGTGCCTGAAGCAAGAATCCTGGAGCTACAGGGACA
 GGGAGCCATCATTCCTGCCTGGGAATCCTGGAAGACTTCTGCAGGAGTCAGCGTTCAATCTTGACCTTGAAGAT
 GGAAGGATGTTCTTTTTACGTACCAATTCTTTTGTCTTTTGATATTAAGAAAGAGTACATGTTTCATTGTAGAGA
 ATTTGGAAGTGTAGAAGAGAATCAAGAAGAAAAATAAAATCAGCTGTTGTAATCGCCTAGCAAAAAAAAAAAAA
 AA

09978187 101501

FIGURE 204

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50921

<subunit 1 of 1, 693 aa, 1 stop

<MW: 77738, pI: 8.87, NX(S/T): 7

MTPQSLQLQTTLFLLSLLFLVQGAHGRGHREDFRFGCSQRNQTHRSSLHYKPTPDLRISIENSE
EALT VHAPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGKRDFLLSDKASSLLCFQH
QEESLAQGPPLLATSVTSWWSPQNISLPSAASFTFSFHSPHTAAHNASVDMCELKRDLQLL
SQFLKHPQKASRRPSAAPASQQQLQSLESKLTSVRFMGDMVSFEEDRINATVWKLQPTAGLQD
LHIHSRQEEEQSEIMEYSVLLPRTL FQRTKGRSGEAEKRLLLVDFSSQALFQDKNSSQVLGE
KVLGIVVQNTKVANLTEPVVLT FQHQLQPKNVT LQCVFWVEDPTLSSPGHWSSAGCETVRRE
TQTSCFCNHLTYFAVLMVSSVEVDAVHKHYLSLLSYVGCVVVSALACLV TIAAYLCSRVP LPC
RRKPRDYTIKVH MNLLLAVFLLDTSFLLSEPVALTGSEAGCRASAI FLHFSLLTCLSWMGLE
GYNLYRLVVEVFGTYVPGYLLKLSAMGWGFPI FLVTLVALVDVDNYGPI ILAVHRTPEGVIY
PSMCWIRDSLVS YITNLGLFSLVFLFN MAMLATMVVQILRLRPHTQKWSHVL TLLGLSLVLG
LPWALIFFSFASGTFQLVVLYLFSIITSFQGFLIFIWYWSMRLQARGGPSPLKSNSDSARLP
ISSGSTSSSRI

Important features:

Signal peptide:

amino acids 1-25

Putative transmembrane domains:

amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590
and 634-657

Microbodies C-terminal targeting signal.

amino acids 691-693

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 198-201 and 370-373

N-glycosylation sites.

amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327
and 341-344

G-protein coupled receptors family 2 proteins

amino acids 475-504

FIGURE 205

TGCCTGGCCTGCCTTGTCAACAATGCCGCTTACTCTGCTTCCAGGTTGCCCTGCCTTGCAGA
GGAAANCNTCGGGACTACACCNTCAAGTGCACATGAACCTGCTGCTGGCCGTCTTCCTGCTG
GACACGAGCTTCCTGCTCAGCGNAGCCGGTGGCCCTGACAGGCTCTGAAGGCTGGCTGCCGA
GCCAGTGCCATCTTCCTGCACTTCTCCTGCTCACCTGCCTTTCCTGGATGGGCCTCGAGGGG
TACAACCTCTACCGACTCGTGGTGGAGGTCTTTGGCACCTATGTCCCTGGCTACCTACTCAA
GCTGAGCGCCATGGGCTGGGGCTTCCCCATCTTTCTGGTGACGCTGGTGGCCCTGGTGGATG
TGGACAACTATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAGGGCGTCATCTACCCT
TCCATGTGCTGGATCCGGGACTCCCTGGTCAGCTACATCACCAACCTGGGCCTCTTCAGCCT
GGTGTTCCTGTTCAACATGG

09978187-10150
T05T0T-28TBZ660

FIGURE 206

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGTTTCAGGTCACAGGTTTTGCTTTGA
TCCTTTTCAAAAACCTGGAGACACAGAAGAGGGCTCTAGGAAAAAGTTTTGGATGGGATTATGTGGAAACTACCCT
GCGATTCTCTGCTGCCAGAGCAGGCTCGGCGCTTCCACCCAGTGCAGCCTTCCCCTGGCGGTGGTGAAAGAGAC
TCGGGAGTCTGCTGCTTCCAAAGTGCCCGCCGTGAGTGAGCTCTCACCCAGTCAGCCAAATGAGCCTCTTCGGGC
TTCTCCTGCTGACATCTGCCCTGGCCGGCCAGAGACAGGGGACTCAGGCGGAATCCAACCTGAGTAGTAAATTCC
AGTTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAATTATTACTGTGTCTACTAATG
GAAGTATTCACAGCCCCAAGGTTTCTCTACATTTATCCAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAG
AGGAAAATGTATGGATACAACCTTACGTTTGATGAAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGT
ATGATTTTGTAGAAGTTGAGGAACCCAGTGATGGAATATATTAGGGCGCTGGTGTGGTTCTGGTACTGTACCAG
GAAAACAGATTTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTCTCTTGAACCAGGGT
TCTGCATCCACTACAACATTGTCTATGCCACAATTCACAGAAGCTGTGAGTCCTTCAGTGCTACCCCTTCAGCTT
TGCCACTGGACCTGCTTAATAATGCTATAACTGCCCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACCAG
AGAGATGGCAGTTGGACTTAGAAGATCTATATAGGCCAAGTGGCAACTTCTTGGCAAGGCTTTTGTTCCTTGGAA
GAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCT
CAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTG
GTGGGAACCTGTGCCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACC
ACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTGAGGGGATTGCACAAATCACTCACCGACGTGGCCCTGGAGC
ACCATGAGGAGTGTGACTGTGTGTGTCAGAGGGAGCACAGGAGGATAGCCGCATCACACCAGCAGCTCTTGCCCA
GAGCTGTGCAGTGCAGTGGCTGATTCATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGTCT
TCAAGGACCTTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAAATTAGGAGTTGTGCA
ACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAAATTAATGTTGTAT
TAAATAGATCACCAAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTTTCAGTTCTTTC
GATACGGCTTAGGGTAATGTGAGTACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAAC
TCTAAAGCTCCATGTCTGGGCTTAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTGTCTCATATTCACAT
ATGTAAACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAGGAACATATGTTGCTATGAATTAAACTTGT
GTCATGCTGATAGGACAGACTGGATTTTTTCATATTTCTTATTAAATTTCTGCCATTTAGAAGAAGAGAACTACA
TTCATGGTTTTGGAAGAGATAAACCTGAAAAGAAGAGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTTG
TTTCATTGTGTACATTTTTATATTCTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTAAATATATCT
ATTTTTACCAAAGGTATTTAATATTCTTTTTTATGACAACCTTAGATCAACTATTTTAGCTTGGTAAATTTTTCT
AAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTTCA
TTCTCGTATGGTGCTAGAGTTAGATTAATCTGCATTTTAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAAA
GACTTTTTGAAAATAATTAATATATCATATCTTCCATTCTGTTATTGGAGATGAAAATAAAAAAGCACTTATGA
AAGTAGACATTCAGATCCAGCCATTACTAACCTATTCTTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACAT
AAAGCACCTTGAAAAAGACTTGGCAGCTTCTGTATAAAGCGTGCTGTGCTGTGCAGTAGGAACACATCCTATTTA
TTGTGATGTTGTGGTTTTTATTATCTTAAACTCTGTTCCATACACTTGTATAAATACATGGATATTTTTATGTACA
GAAGTATGTCTCTTAACAGTTCACTTATTGTACTCTGGCAATTTAAAGAAAATCAGTAAAAATTTTTGCTTGT
AAAATGCTTAATATNGTGCCTAGGTTATGTGGTGACTATTTGAATCAAAAATGTATTGAATCATCAAATAAAGA
ATGTGGCTATTTTGGGGAGAAAATTAAAAAAAAAAAAAAAAAAAGGTTTAGGGATAACAGGGTAATGCGGCC

09973137-101501

FIGURE 207

MSLFGLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPR
FPHTYPRNTVLVWRLVAVEENVWIIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWC
GSGTVPKGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLL
NNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLTEEVRLY
SCTPRNFSVSIREELKRDTDFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQ
LRPKTGVRGLHKSLTDVALEHHEECDVCVRGSTGG

Signal sequence:

amino acids 1-14

0978137-101501
TOSTOT-23TB660

FIGURE 208

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTCTGCTCTCTTCAACCAGACCTCTACATTCCATTTTGGGAAGA
 AGACTAAAAATGGTGTTCCTAATGTGGACACTGAAGAGACAAATTCCTATCCTTTTTAACATAATCCTAATTTCC
 AAATCCTTTGGGGCTAGATGGTTTCTTAAACTCTGCCCTGTGATGTCACTCTGGATGTTCCAAAGAACCATGTG
 ATCGTGGACTGCACAGACAAGCATTTGACAGAAATTCCTGGAGGTATTCACACGAACACCACGAACCTCACCTC
 ACCATTAACCACATACCAGACATCTCCCAGCGTCTTTTACAGACTGGACCATCTGGTAGAGATCGATTTTCTAGA
 TGCAACTGTGTACCTATTCCACTGGGGTCAAAAAACAACATGTGCATCAAGAGGCTGCAGATTAAACCCAGAAGC
 TTTAGTGGACTCACTTATTTAAATCCCTTTACCTGGATGGAAACCAGCTACTAGAGATACCGCAGGGCCTCCCG
 CCTAGCTTACAGCTTCTCAGCCTTGAGGCCAAACATCTTTTCCATCAGAAAAGAGAATCTAACAGAACTGGCC
 AACATAGAAATACTTACCTGGGCCAAACTGTTATTATCGAAATCCTTGTATGTTTCATATTCAATAGAGAAA
 GATGCCCTTCTTAACTTGACAAAGTTAAAAGTGCTCTCCCTGAAAGATAACAATGTACAGCCGTCCCTACTGTT
 TTGCCATCTACTTTAACAGAACTATATCTCTACAACAACATGATTGCAAAAAATCCAAGAAGATGATTTTAATAAC
 CTCAACCAATTACAAATTTCTTGACCTAAGTGGAAATTTGCCCTCGTTGTTATAATGCCCCATTTCTTGTGCGCCG
 TGTAAAAATAATTTCTCCCTACAGATCCCTGTAAATGCTTTTGATGCGCTGACAGAATTTAAAGTTTACGTCTA
 CACAGTAACTCTCTCAGCATGTGCCCCAAGATGGTTTAAAGACATCAACAACTCCAGGAACCTGGATCTGTCC
 CAAAACCTTCTGGCCAAAGAAATTTGGGGATGCTAAATTTCTGCATTTCTCCCCAGCCTCATCCAATTGGATCTG
 TCTTTCAATTTTGAACCTTCAGGTCTATCGTGCATCTATGAATCTATCACAAAGCATTTTCTTCACTGAAAAGCCTG
 AAAATTCTGCGGATCAGAGGATATGTCTTTAAAGAGTTGAAAAGCTTTAACCTCTCGCCATTACATAATCTTCAA
 AATCTTGAAGTTCTTGATCTTGGCACTAACTTTATAAAAAATTGCTAACCTCAGCATGTTTAAACAATTTAAAAGA
 CTGAAAGTCATAGATCTTTTCAAGTGAATAAAATATCACCTTCAGGAGATTCAGTGAAGTTGGCTTCTGCTCAAAT
 GCCAGAACTTCTGTAGAAAGTTATGAACCCAGGCTCTGGAACAATTACATTATTTTCAAGATATGATAAGTATGCA
 AGGAGTTGCAGATTCAAAAACAAAGAGGCTTCTTTTATGTCTGTTAATGAAAGCTGCTACAAGTATGGGCAGACC
 TTGGATCTAAGTAAAAATAGTATATTTTGTCAAGTCTCTGATTTTCAAGCATCTTCTTTCTCAATGCTG
 AATCTGTCAAGAAATCTCATTAGCCAACTCTTAATGGCAGTGAATTCACCTTTAGCAGAGCTGAGATATTTG
 GACTTCTCCAACAACCGGCTTGATTTACTCCATTCAACAGCATTTGAAGAGCTTCACAACTGGAAGTTCTGGAT
 ATAAGCAGTAATAGCCATTATTTTCAATCAGAAGGAATTACTCATATGCTAAACTTTACCAAGAACCTAAAGGTT
 CTGCAGAACTGATGATGAACGACAATGACATCTCTTCTCCACCAGCAGGACCATGGAGAGTGAGTCTCTTAGA
 ACTCTGGAATTCAGAGGAAATCACTTAGATGTTTTATGGAGAGAAGGTGATAACAGATACTTACAATTATTCAAG
 AATCTGCTAAATTAGAGGAATTAGACATCTCTAAAAATCCCTAAGTTTCTTGCTTCTGGAGTTTTTGATGGT
 ATGCCTCCAAATCTAAAGAACTCTCTTTGGCCAAAAATGGGCTCAAATCTTTCAGTTGGAAGAACTCCAGTGT
 CTAAAGAACCTGGAACTTTGGACCTCAGCCACAACCACTGACCACTGTCCCTGAGAGATTATCCAAGTGTTC
 AGAAGCCTCAAGAATCTGATTCTTAAGAATAATCAAATCAGGAGTCTGACGAAGTATTTTCTACAAGATGCCTTC
 CAGTTGCGATATCTGGATCTCAGCTCAAATAAAATCCAGATGATCCAAAAGACCAGCTTCCCAGAAAATGTCCTC
 AACAACTGAAGATGTTGCTTTTGCATCATAATCGGTTTCTGTGCACCTGTGATGCTGTGTGGTTTGTCTGGTGG
 GTTAACCATACGGAGGTGACTATTCCTTACCTGGCCACAGATGTGACTTGTGTGGGGCCAGGAGCACACAAGGGC
 CAAAGTGTGATCTCCCTGGATCTGTACACCTGTGAGTTAGATCTGACTAACCTGATTCTGTTCTCACTTTCCATA
 TCTGTATCTCTTTTCTCATGGTGATGATGACAGCAAGTCACCTCTATTTCTGGGATGTGTGGTATATTTACCAT
 TTCTGTAAGGCCAAGATAAAGGGGTATCAGCGTCTAATATCACCAGACTGTTGCTATGATGCTTTTATTGTGTAT
 GACACTAAAGACCCAGCTGTGACCGAGTGGGTTTTGGCTGAGCTGGTGGCCAACTGGAAGACCCAAAGAGAGAAA
 CATTTTAATTTATGTCTCGAGGAAAGGGACTGGTTACCAGGGCAGCCAGTTCTGGAACCTTTCCAGAGCATA
 CAGCTTAGCAAAAAGACAGTGTGTTGTGATGACAGACAAGTATGCAAGACTGAAAATTTTAAAGATAGCATTTTAC
 TTGTCCCATCAGAGGCTCATGGATGAAAAAGTTGATGTGATTATCTTGATATTTCTTGAGAAGCCCTTTTCAAG
 TCCAAGTTCTCCAGCTCCGGAAAAGGCTCTGTGGGAGTTCTGTCTTGAAGTGGCCAAACAAACCCGCAAGCTCAC
 CCATACTTCTGGCAGTGTCTAAAGAACGCCCTGGCCACAGACAATCATGTGGCCTATAGTCAGGTGTTCAAGGAA
 ACGGTCTAGCCCTTCTTTGCAAAACACAACCTGCCTAGTTTACCAAGGAGAGGCCTGGC

09973137 101504

FIGURE 209

MVFPMWTLKRQILILFNIILISKLLGARWFPKTLPCDVTLDVPMKNHVIVDCTDKHLTEIPGG
IPTNTTNLTTLTINHIPDISPASFHRLDHLVEIDFRNCNCPVPIPLGSKNNMCIKRLQIKPRSFS
GLTYLKSLYLDGNQLLEIPQGLPPSLQLLSLEANNIFSIRKENLTELANIEILYLGQNCYYR
NPCYVSYSIEKDAFLNLTKLKVLSLKDNNVTAVPTVLPSTLTELYLYNNMIAKIQEDDFNNL
NQLQILDLSGNCPRCYNAPFPCAPCKNNSPLQIPVNAFDALTELKVLRLHSNSLQHVPPRWF
KNINKLQELDLSQNFLAKEIGDAKFLHFLPSLIQLDLSFNFELQVYRASMNLSQAFSSLKSL
KILRIRGYVFKELKSFNLSPLHNLQNLEVLDLGTNFIKIANLSMFKQFKRLKVIDLSVNKIS
PSGDSSEVGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGO
TLDLSKNSIFFVKSSDFQHLNFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNNRLDLLH
STAFEELHKLEVLDISSNSHYFQSEGITHMLNFTKNLKVLQKLMMNDNDISSSTSRTMESES
LRTLEFRGNHLDVLWREGDNRYLQLFKNLLKLEELDISKNLSLFLPSGVFDGMPPNLKNLSL
AKNGLKSFSWKKLQCLKNLETLDLSHNQLTTVPERLSNCSRSLKNLILKNNQIRSLTKYFLQ
DAFQLRYLDLSSNKIQMIQKTSFPENVLNNLKMLLLHHRFLCTCDAVWFVWWVNHTVETIP
YLATDVTCVGPGAHKGQSVISLDLYTCELDLTNLILFSLSISVSLFLMVMMTASHLYFWDVW
YIYHFCKAKIKGYQRLISPDCCYDAFIVYDTKDPVTEWVLAELVAKLEDPREKHFNLCLEE
RDWLPGQPVLENLSQSIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVILIFLE
KPFQKSKFLQLRKRLCGSSVLEWPTNPQAHFYFWQCLKNALATDNHVAYSQVFKETV

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 840-860

FIGURE 210

GGGTACCATTCTGCGCTGCTGCAAGTTACGGAATGAAAAATTAGAACAACAGAAACATGGAAAAATGTTCCCTTC
 AGTCGTCAATGCTGACCTGCATTTTCTGCTAATATCTGGTTCTGTGAGTTATGCGCCGAAGAAAAATTTTCTA
 GAAGCTATCCTTGTGATGAGAAAAAGCAAAATGACTCAGTTATTGCAGAGTGCAGCAATCGTCGACTACAGGAAG
 TTCCCCAAACGGTGGGCAAAATATGTGACAGAACTAGACCTGTCTGATAATTTTATCACACACATAACGAATGAAT
 CATTTCAAGGGCTGCAAAATCTCACTAAAAATAAATCTAAACCACAACCCCAATGTACAGCACCAGAACGGAAATC
 CCGGTATACAATCAAATGGCTTGAATATCACAGACGGGGCATTCCTCAACCTAAAAAACCTAAGGGAGTTACTGC
 TTGAAGACAACCAGTTACCCCAAATACCCTCTGGTTTGCCAGAGTCTTTGACAGAACTTAGTCTAATTCAAAACA
 ATATATACAACATAACTAAAGAGGGCATTTCAAGACTTATAAACTTGAAAAATCTCTATTTGGCCTGGAACCTGCT
 ATTTTAAACAAAGTTTGGGAGAAAACTAACATAGAAGATGGAGTATTTGAAACGCTGACAAATTTGGAGTTGCTAT
 CACTATCTTTCAATTCTCTTTACACGTGCCACCCAAACTGCCAAGCTCCCTACGCAAACTTTTCTGAGCAACA
 CCCAGATCAAATACATTAGTGAAGAAGATTTCAAGGGATTGATAAATTTAACATTACTAGATTTAAGCGGGAAC
 GTCCGAGGTGCTTCAATGCCCCATTTCCATGCGTGCCTTGTGATGGTGGTGCCTTCAATTAATATAGATCGTTTTG
 CTTTTCAAACTTGACCCAACTTCGATACCTAAACCTCTCTAGCACTTCCCTCAGGAAGATTAATGCTGCCTGGT
 TTAATAATATGCCTCATCTGAAGGTGCTGGATCTTGAATTTCACTATTTAGTGGGAGAAATAGTCTCTGGGGCAT
 TTTTAAACGATGCTGCCCGCTTAGAAATACTTGACTTGTCTTTTAACTATATAAAGGGGAGTTATCCACAGCATA
 TTAATATTTCCAGAACTTCTCTAACTTTTGTCTCTACGGGCATTGCATTTAAGAGGTTATGTTTCCAGGAAC
 TCAGAGAAGATGATTTCCAGCCCCTGATGCAGCTTCCAACTTATCGACTATCAACTTGGGTATTAATTTTATTA
 AGCAAATCGATTTCAAACCTTTTCCAAATTTCTCCAATCTGGAAATTTATTTACTTGTGAGAAACAGAATATCAC
 CGTTGGTAAAAGATACCCGGCAGAGTTATGCAAATAGTTCCCTCTTTTCAACGTCTATATCCGGAACGACGCTCAA
 CAGATTTTGAATTTGACCCACATTCGAACTTTTATCATTTTACCCCGTCCCTTAAATAAAGCCACAATGTGCTGCTT
 ATGGAAGGCCCTTAGATTTAAGCCTCAACAGTATTTCTTCAATTTGGGCCAAACCAATTTGAAAACTTCTCTGACA
 TTGCCTGTTTAAATCTGTCTGCAATAGCAATGCTCAAGTGTAAAGTGGAACTGAATTTTTCAGCCATTCCTCATG
 TCAAATATTTGGATTTGACAAACAATAGACTAGACTTTGATAATGCTAGTGTCTTACTGAATTTGTCGAGCTTGG
 AAGTTCTAGATCTCAGCTATAATTCACACTATTTCAGAATAGCAGGCGTAACACATCATCTAGAATTTTATTCAAA
 ATTTACAAATCTAAAAGTTTTTAACTTGAGCCACAACAACATTTTATACTTTAACAGATAAGTATAACCTGGAAA
 GCAAGTCCCTGGTAGAATTAGTTTTTCAAGTGGCAATCGCCTTGACATTTTGTGGAATGATGATGACAACAGGTATA
 TCTCCATTTTCAAAGGTCTCAAGAATCTGACACGTCTGGATTTATCCCTTAAATAGGCTGAAGCACATCCCAAATG
 AAGCATTCCTTAAATTTGGCAGCGAGTCTCACTGAACCTACATATAAATGATAATATGTTAAAGTTTAACTGGA
 CATTACTCCAGCAGTTTCTCGTCTCGAGTTGCTTGACTTACGTGGAAACAACTACTCTTTTAACTGATAGCC
 TATCTGACTTTTACATCTTCCCTTCCGACACTGCTGCTGAGTCATAACAGGATTTCCACCTACCTCTGGCTTTT
 TTTCTGAAGTCAGTAGTCTGAAGCACCTCGATTTAAGTTCCAATCTGCTAAAAACAATCAACAAATCCGCACTTG
 AAATAAGACCACCACCAATTTATCTATGTTGGAATACACGGAACCCCTTTGAATGCACCTGTGACATTTGGAG
 ATTTCCGAAGATGGATGGATGAACATCTGAATGTCAAATTTCCAGACTGGTAGATGTCAATTTGTGCCAGTCCCTG
 GGGATCAAAGAGGGAAGAGTATTGTGAGTCTGGAGCTAACCACTTGTGTTTTCAGATGTCACTGCAGTGATTTAT
 TTTTCTTACAGTTTCTTTATCACCACCATGGTTATGTTGGCTGCCCTGGCTCACCATTGTGTTTACTGGGATGTTT
 GGTTTATATATAATGTGTGTTTAGCTAAGGTAAAAGGCTACAGGTCTCTTTCCACATCCCAAATTTCTATGATG
 CTTACATTTCTTATGACACCAAAGATGCCTCTGTTACTGACTGGGTGATAAATGAGCTGCGCTACCACCTTGAAG
 AGAGCCGAGACAAAAACGTTCTCCTTTGTCTAGAGGAGAGGGATTGGGACCCGGGATTGGCCATCATCGACAACC
 TCATGCAGAGCATCAACCAAAGCAAGAAAAAGTATTTGTTTTAACCAAAAAATATGCAAAAAGCTGGAACTTTA
 AAACAGCTTTTTTACTTTGGCTTTGAGAGGCTAATGGATGAGAACATGGATGTGATTATATTTATCCTGCTGGAGC
 CAGTGTACAGCATTCTCAGTATTTGAGGCTACGGCAGCGGATCTGTAAGAGCTCCATCCTCCAGTGGCCTGACA
 ACCCGAAGGCAGAAAGGCTTGTGTTTGGCAAATCTGAGAAATGTGGTCTTGACTGAAAATGATTACGGTATAACA
 ATATGTATGTCGATTCCATTAAAGCAATACTAACTGACGTTAAGTCATGATTTTCGCGCCATAATAAAGATGCAAAG
 GAATGACATTTCTGTATTAGTTATCTATTGCTATGTAACAAATTTATCCCAAACCTTAGTGGTTTTAAACCAACACA
 TTTGCTGGCCACAGTTTTTGGGGTCAAGAGTCCAGGCCAGCATAACTGGGTCTCTGCTCAGGGTGTCTCAG
 AGGCTGCAATGTAGGTGTTTACCAGAGACATAGGCATCACTGGGTGTTTCTGATGTTTCTGATTTTCTGATTTCA
 ATTCTCTGGGCTATTGGCCAAAGGCTATACTCATGTAAGCATGCGAGCCTCTCCACAAGGCAGCTTGCTTC
 ATCAGAGCTAGCAAAAAAGAGAGGTTGCTAGCAAGATGAAGTCACAATCTTTTGTAAATCGAATCAAAAAAGTGAT
 ATCTCATCACTTTGGCCATATTCTATTTGTTAGAAGTAAACACAGGTCCACCAGCTCCATGGGAGTGACCACC
 TCAGTCCAGGGAAAACAGCTGAAGACCAAGATGGTGAGCTCTGATTGCTTCAGTTGGTTCATCAACTATTTTCCCT
 TGACTGCTGCTGGGATGGCCTGCTATCTTGATGATAGATTGTGAATATCAGGAGGCAGGGATCACTGTGGACC
 ATCTTAGCAATGACCTAACACATCTTCTTTCAATATCTAAGAACTTTTGGCACTGTGACTAATGGTCTTAATA
 TTAAGCTGTTGTTTATATTTATATCTATCTATGCTACATGTTTATATTATGCTGTGGTTGCGTTTCTGTTTAT
 TTACAGTTGCTTTTACAAATATTTGCTGTAACATTTGACTTCTAAGGTTTAGATGCCATTTAAGAAGTGAAGATGG
 ATAGCTTTTAAAGCATCTTTTACTTCTTACCATTTTTTAAAGATATGCAGCTAAATTCGAAGCTTTTGGTCTATA
 TTGTTAATTGCCATTTGCTGTAAATCTTAAATGAATGAATAAAAAATGTTTCAATTTTACAAAAA

FIGURE 211

MENMFLQSSMLTCIFLLISGSCELCAEENFSRSYPCDEKKQNDSVIAECSNRRLQEVPTVG
KYVTELDLSDNFITHITNESFQGLQNLTKINLNHNPNVQHQNNGNPGIQSNGLNITDGAFLNL
KNLRELLLEDNQLPQIPSGLPESLTELSLIQNNIYNITKEGISRLINLKNLYLAWNCYFNKV
CEKTNIEDGVFETLTNLELLSLSFNSLSHVPPKLPSSLRKLFLSNTQIKYISEEDFKGLINL
TLLDLSGNCPRCFNAPFPCVPCDGGASINIDRFQNLTLQLRYLNLSSTSLRKINAAWFKNM
PHLKVLDLEFNVLVGEIVSGAFLTMLPRLEILDLSFNLIKGSYPQHINISRNFSKLLSLRAL
HLRGYVFQELREDDFQPLMQPLPNLSTINLGINFIKQIDFKLFQNFNLEIIYLSENRISPLV
KDTRQSYANSSSFQRHIRKRRSTDFFEDPHSNFYHFTRPLIKPQCAAYGKALDLSLNSIFFI
GPNQFENLPDIACLNLSANSNAQVLSGTEFSAIPHVKYLDLTNNRLDFDNASALTELSDELEV
LDLSYNSHYFRIAGVTHHLEFIQNFTNLKVLNLSHNNIYTLTDKYNLESKSLVELVFSGNRL
DILWNDDDNRYISIFKGLKNLTRLDLSLNRLKHIPNEAFLNLPASLTEHINDNMLKFFNWT
LLQQFPRELLDLRGNKLLFLTDSLSDFTSSLRTLLLSHNRISHLPSGFLSEVSSLKHLDL
SNLLKTINKSALETKTTTKLSMLELHGPNPFECTCDIGDFRRWMDEHLNVKIPRLVDVICASP
GDQRGKSIVSLELTTCVSDVTAVILFFFITTTMVMLAALAHHLFYWDVWFIYNVCLAKVK
GYRSLSTSQTIFYDAYISYDTKDASVTDWVINELRYHLEESRDKNVLLCLEERDWDPLAIIID
NMQSINQSKKTVFVLTKKYAKSWNFKTA FYLALQRLMDENMDVIIIFILLEPVLQHSQYLRL
RQRICKSSILQWPDNPKAEGLEFWQTLRNVLTLTENDSRYNNMYVDSIKQY

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 826-848

FIGURE 212

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCT
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA
CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGC
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGA
GCAGCTCCTGCCCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAA
GGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTT
CTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGTGCTGT
CCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTTCGTGCAGCGTGTGTACCAGCCCTTCCTCA
CCACCTGCGACGGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGC
CGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAGGAC
CAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGA
GCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCA
GATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCATCAACACCGCCGG
CAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGC
CCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAGGAA
GAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCTGGC
CCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCC
TGGTGCACCTCCTTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTCTCCTG
GAGGAGCAGCTGGGGTCCTGCTCCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGGCTG
GACTGAGCCCCTCACGCCGCCCTGCAGCCCCCATGCCCCTGCCCAACATGCTGGGGGTCCAG
AAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTCTTCCTCCTCCCC
TTCCTCGGGAGGCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCAC
CCCTGGCTACCCCCACCCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTG
AGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAG
GCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACATAAAAAATGAAACGTGA
AAAGGGCGGCCGCGACTCTAGAGT
CGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAAT

FIGURE 213

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDVSESVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCVPKGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

09978187.101501
TOSTOT/8TB/660

FIGURE 214

GCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAG
GGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCC
AGCAGCATCAGAGCAGCCCCCTGTGGTTGGCAGCAAAGTTTCAGCTTGGCTGGGCCCCGCTGTGA
GGGGCTTCGCGCTACGCCCTGCGGTGTCCCGAGGGCTGAGGTCTCCTCATCTTCTCCCTAGC
AGTGGATGAGCAACCCAACGGGGGGCCCGGGGAGGGGAAGTGGCCCCGAGGGAGAGGAACCCC
AAAGCCACATCTGTAGCCAGGATGAGCAGTGTGAATCCAGGCAGCCCCCAGGACCGGGGAGG
CACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGCCCTGTCCGGGGGATGACTGATTTC
TCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGC
TCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTA
CCGGCCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTTCG
TGCAGCGTGTGTACCAGCCCTTCCTCACCACTGCGACGGGCACCGGGCCTGCAGCACCTAC
CGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTA
CGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATAT
GCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCA
GGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGCTAGGAGGGGGCGGCTG
TCCCCAGCGCTGCATCAACACCGCCGGCAGTTACTGGTGCCAGTGTTGGGAGGGGGCACAGCC
TGTCTGCAGACGGTACACTCTGTGTGCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCG
ACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCT
GGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGC
ATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACTCCTTCCAGCAGCTCGGCCGCATCGAC
TCCCTGAGCGAGCAGATTTCTTCCTGGAGGAGCAGCTGGGGTCTTGCTCCTGCAAGAAAGA
CTCGTGACTGCCCAGCGCTCCAGGCTGGACTGAGCCCCTCACGCCGCCCTGCAGCCCCCATG
CCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGC
AGGGCCTTCCTCCTCTTCCTCCTCCCCTTCCTCGGGAGGCTCCCCAGACCCTGGCATGGGAT
GGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACCCCCACCCTGGCTACCCCAACGGCA
TCCCAAGGCCAGGTGGACCCTCAGCTGAGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGAC
CCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGAC
CCCCAGCACAATAAAAATGAAACGTG

FIGURE 215

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCVPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

09978187-101501
TOSTOT-8TB/660

FIGURE 216

CCCACGCGTCCGAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGACAGGCCAGGCA
GGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAGGGCTAGGG
TCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCCAGCAGCAT
CAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGC
CCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGC
CTGGAGGCACAGGCCATGAGGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTTGGC
AGTGGGCGGCACAGAGCACGCCTACCGGCCCGCCGTAGGGTGTGTGCTGTCCGGGCTCACG
GGGACCCTGTCTCCGAGTCGTTTCGTGCAGCGTGTGTACCAGCCCTTCCTCACCACCTGCGAC
GGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGG
GCTGGCCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTC
CTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAG
CCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGA
ATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCGTCAACACCGCCGGCAGTTACTGGT
GCCAGTGTTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGG
CCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAG
GCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACA
GCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACTCC
TTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTCCTGGAGGAGCAGCT
GGGGTCCTGCTCCTGCAAGAAAGACTCGTGACTGCCAGCGCCCCAGGCTGGACTGAGCCCC
TCACGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCG
GGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTCTTCCTCCTCCCCCTTCCTCGGGAG
GCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACC
CCCACCCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTGAGGGAAGGTAC
GAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGG
CCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACAATAAAAATGAAACGTG

FIGURE 217

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCQSDVDECSARRGGCPQRCVNTAGSYWCQCWEGHSLSADGTLCVPKGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKDS

Signal sequence:

1-19

09978187-101501
TOTAL 287860

FIGURE 218

GGTTGCCACAGCTGGTTTTAGGGCCCCGACCCTGCGGGCCCTTGTGAGGAGGAGACAGCCTCCCGGCCCGGGGAG
GACAAGTCGCTGCCACCTTTGGCTGCCGACGTGATTCCCTGGGACGGTCCGTTTCTGCGCTCAGCTGCCGGCCG
AGTTGGGTCTCCGTGTTTCAGGCCGGCTCCCCCTTCTGGTCTCCCTTCTCCCGCTGGGCCGGTTTTATCGGGAGG
AGATTGTCTTCCAGGGCTAGCAATTGGACTTTTGATGATGTTTGACCCAGCGGCAGGAATAGCAGGCAACGTGAT
TTCAAAGCTGGGCTCAGCCTCTGTTTCTTCTCTCGTGAATCGCAAAACCCATTTTGGAGCAGGAATCCAATCA
TGTCTGTGATGGTGGTGAGAAAGAAGGTGACACGGAAATGGGAGAACTCCCAGGCAGGAACACCTTTTGCTGTG
ATGGCCCGCTCATGATGGCCCCGGCAAAAGGGCATTTTCTACCTGACCCTTTTCTCATCCTGGGGACATGTACAC
TCTTCTTCGCCTTTGAGTGCCGCTACCTGGCTGTTCAGCTGTCTCCTGCCATCCCTGTATTTGCTGCCATGCTCT
TCCTTTTCTCCATGGCTACACTGTTGAGGACCAGCTTCAGTGACCCTGGAGTGATTCTCGGGCGCTACCAGATG
AAGCAGCTTTTCATAGAAATGGAGATAGAAGCTACCAATGGTGCGGTGCCCCAGGGCCAGCGACCACCGCCTCGTA
TCAAGAATTTCCAGATAAAACAACCAGATTGTGAAACTGAAATACTGTTACACATGCAAGATCTTCGGGCCCTCCCC
GGGCCTCCCATTTGCAGCATCTGTGACAACTGTGTGGAGCGCTTCGACCATCACTGCCCCCTGGGTGGGGAATTGTG
TTGGAAAGAGGAACCTACCGCTACTTCTACCTCTTCATCCTTTCTCTCTCCCTCCTCACAATCTATGTCTTCGCCT
TCAACATCGTCTATGTGGCCCTCAAATCTTTGAAAATTGGCTTCTTGGAGACATTGAAAAGAACTCCTGGAACCTG
TTCTAGAAGTCTCATTTGCTTCTTTACACTCTGGTCCGTCTGTTGGGACTGACTGGATTTCACTTTTCTCGTGG
CTCTCAACCAGACAACCAATGAAGACATCAAAGGATCATGGACAGGGAAGAATCGCGTCCAGAATCCCTACAGCC
ATGGCAATATTGTGAAGAACTGCTGTGAAGTGCTGTGTGGCCCCCTGCCCCCAGTGTGCTGGATCGAAGGGGTA
TTTTGCCACTGGAGGAAAGTGAAGTCGACCTCCCAGTACTCAAGAGACCAGTAGCAGCCTCTTGCCACAGAGCC
CAGCCCCCACAGAACACCTGAACTCAAATGAGATGCCGGAGGACAGCAGCACTCCCGAAGAGATGCCACCTCCAG
AGCCCCCAGAGCCACCACAGGAGGCAGCTGAAGCTGAGAAGTAGCCTATCTATGGAAGAGACTTTTGTTTGTGTT
TAATTAGGGCTATGAGAGATTTAGGTGAGAAGTTAAACCTGAGACAGAGAGCAAGTAAGCTGTCCCTTTTAACT
GTTTTTCTTTGGTCTTTAGTCACCCAGTTGCACACTGGCATTTTCTTGCTGCAAGCTTTTTTAAATTTCTGAACT
CAAGGCAGTGGCAGAAGATGTCAGTCACCTCTGATAACTGGAAAAATGGGTCTCTTGGGCCCTGGCACTGGTTCT
CCATGGCCTCAGCCACAGGGTCCCCCTTGGACCCCCCTCTCTTCCCTCCAGATCCAGCCCTCCTGCTTGGGGTCAC
TGGTCTCATTCTGGGGCTAAAAGTTTTTGAGACTGGCTCAAATCCTCCCAAGCTGCTGCACGTGCTGAGTCCAGA
GGCAGTCACAGAGACCTCTGGCCAGGGGATCCTAAGTGGGTCTTGGGGTCTTCAGGACTGAAGAGGAGGGAGAG
TGGGGTCAGAAGATTCTCCTGGCCACCAAGTGCCAGCATTGCCCAAAATCCTTTTAGGAATGGGACAGGTACCT
TCCACTTGTTGTANNNNNNNNNNNNNNNNNNNNNNNNNNNNTTGTTTTTTCTTTTGACTCCTGCTCCCATTAGGAG
CAGGAATGGCAGTAATAAAAGTCTGCACCTTTGGTCAATTTCTTTTCTCAGAGGAAGCCCGAGTGCTCACTTAAAC
ACTATCCCCTCAGACTCCCTGTGTGAGGCCCTGCAGAGGCCCTGAATGCACAAATGGGAAACCAAGGCACAGAGAG
GCTCTCCTCTCCTCTCCTCTCCCCCGATGTACCTCAAACCAACCAATGCTAACCAGTTCTTCCATTAAAGCCT
CGGCTGAGTGAGGGAAGCCAGCACTGCTGCCCTCTCGGGTAACTCACCTAAGGCCTCGGCCACCTCTGGCT
ATGGTAACCACACTGGGGGCTTCTCCAAGCCCCGCTCTTCCAGCACTTCCACCGGCAGAGTCCCAGAGCCACTT
CACCTGGGGGTGGGCTGTGGCCCCAGTCAGCTCTGCTCAGGACCTGCTCTATTTAGGGAAGAAGATTTATGT
ATTATATGTGGCTATATTTCTAGAGCACCTGTGTTTTCTCTTTCTAAGCCAGGGTCTGTCTGGATGACTTAT
GCGGTGGGGGAGTGTAACCGGAACTTTTCATCTATTTGAAGGCGATTAAACTGTGTCTAATGCA

FIGURE 219

MSVMVVRKKVTRKWEKLPGRNTFCCDGRVMMARQKGIFYLTLFLILGTCTLFFAFECRYLAV
QLSPAIPVFAAMLFLFSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPP
RIKNFQINNQIVKLKYCYTCKIFRPPRASHCSICDNCVERFDHHCWPVGNVCVGKRNYRYFYL
FILSLSLTIYVFAFNIVYVALKSLKIGFLETLKETPGTVLEVLI CFFTLWSVVGLTGFHTF
LVALNQTTNEDIKGSWTGKNRVQNPYSHGNIVKNCCEVL CGPLPPSVLDRRGILPLEESGSR
PPSTQETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPPEPPEPPQEAAEAEK

Putative transmembrane domains:

amino acids 36-55 (type II TM), 65-84, 188-208, 229-245

09978137-101501
TOSTOT-28784660

FIGURE 220

AAAACCCTGTATTTTTTACAATGCAAATAGACAATNANCCTGGAGGTCTTTGAATTAGGTAT
TATAGGGATGGTGGGGTTGATTTTTNTTCCTGGAGGCTTTTGGCTTTGGACTCTCNCTTTCT
CCCACAGAGCNCTTCGACCATCACTGCCCCCTGGGTGGGGAATTGTGTTGGAAAGAGGAACTA
CCGCTANTTCTACCTCTTCATCCTTTNTCTCTCCNCCTCACAATCTATGTCTTCGCCTTCA
ACATCGT

09978187 .101501

FIGURE 221

GTTGTGTCCTTCAGCAAAACAGTGGATTTTAAATCTCCTTGCACAAGCTTGAGAGCAACACAA
TCTATCAGGAAAGAAAGAAAGAAAAAACCGAACCTGACAAAAAGAAGAAAAAGAAGA
AAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGAGAGCGCCACCCTCAGGTGCACTATT
GACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA
CAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCG
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC
CACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTTGTAGAGATTTT
TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGAC
GAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC
CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTACCGTGAACATCCACCATACA
TTTCAGAAGCCAAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC
TCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA
GAAAGGGGTGAAAGTGGAAAACAGACCTTTCTCTCAAACTCATCTTCTTCAATGTCTCTG
AACATGACTATGGGAACTACACTTGCCTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGC
ATCATGCTATTTGGTCCAGGCGCCGTGAGCGAGGTGAGCAACGGCACGTGAGGAGGGCAGG
CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGACCTGCTTCTCAAATTTTGAATGTGAGTGCC
ACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACAC
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA
AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAA
AATTGCCTTGACAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGC
ACACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAA
GGGCTCAGCCTCTCTGCCCACAGAGTGCCCCCAGTGGAACATTCTGGAGCTGGCCATCCCA
AATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGG
GCACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAA
AAAAA

FIGURE 222

MKTIQPKMHNSISWAI FTGLAALCLFQGVPVRS GDATFPKAMDNVTVRQGESATLRCTIDNR
VTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPK
TSRVHLIVQVSPKIVEISSDISINEGNNISLT CIATGRPEPTVTWRHISPKAVGFVSEDEYL
EIQGITREQSGDYEC SASNDVAAPV VRRVKVT VNYPPYISEAKGTGVPVGQKGT LQCEASAV
PSAEFQWYKDDKRLIEGKKG VKVENRPFLSKLIFFNVSEHDYGN YTCVASNKLGH TNASIML
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLL LKF

Signal peptide:

amino acids 1-28

09973187.101501

FIGURE 223

GAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTC
ACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTT
CCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTA
TTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAAT
GACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCAT
CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACA
ACCACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTGTAGAGATT
TCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAG
ACCAGAG

09978187 101501

FIGURE 224

ATGGCTGGTGACGGCGGGGCCGGGCAGGGGACCGGGGCCGCGGGCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGA
ATCACCGCCTGGCCCGACTCCACCATGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAG
AAGGGGACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTACTGCTGGCT
GCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCATCCCACAGCACCTGCCTTACA
GAGGCCTGCATTGAGTGGCTGGAAAAATCCTGGAGTCCCTGGACCGAGGGGTGAGCCCCTGTGAGGACTTTTAC
CAGTTCTCCTGTGGGGCTGGATTTCGGAGGAACCCCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGC
CTCTGGGACCAAAACCAGGCCATACTGAAGCACCTGCTTGAAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAG
CAGAAGACACAGCGCTTCTACCTATCTTGCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCCAGCCACTGAGA
GACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAGGACAACTTTATGGAGGTGTTGAAG
GCAGTAGCAGGGACCTACAGGGCCACCCCATTTCTCACCGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGC
AATGTTATCCAGGTGGACCAGTCTGGGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAG
AAAGTGCTCACTGCCTATCTGGATTACATGGAGGAACTGGGGATGCTGCTGGGTGGGCGGCCACCTCCACGAGG
GAGCAGATGCAGCAGGTGCTGGAGTTGGAGATACAGCTGGCCAACATCACAGTGCCCCAGGACCAGCGCGCGAC
GAGGAGAAGATCTACCACAAGATGAGCATTTCCGAGCTGCAGGCTCTGGCGCCCTCCATGGACTGGCTTGAGTTC
CTGTCTTTCTTGTGTCACTATTGGAGTTGAGTGACTCTGAGCCTGTGGTGGTGTATGGGATGGATTATTTGCAG
CAGGTGTCAGAGCTCATCAACCGCACGGAACCAAGCATCTTGAACAATTACCTGATCTGGAACCTGGTGCAAAAG
ACAACCTCAAGCCTGGACCGACGCTTTGAGTCTGCACAAGAGAAGCTGCTGGAGACCCTCTATGGCACTAAGAAG
TCCTGTGTGCCGAGGTGGCAGACCTGCATCTCCAACACGGATGACGCCCTTGGCTTTGCTTTGGGGTCACTCTTC
GTGAAGGCCACGTTTGAACCGCAAAGCAAAGAAATTGCAGAGGGGATGATCAGCGAAATCCGGACCGCATTGAG
GAGGCCCTGGGACAGCTGGTTTGGATGGATGAGAAGACCCGCCAGGCAGCCAAGGAGAAAGCAGATGCCATCTAT
GATATGATTGGTTTCCCAGACTTTATCCTGGAGCCCAAAGAGCTGGATGATGTTTATGACGGGTACGAAATTTCT
GAAGATTCTTTCTTCCAAAACATGTTGAATTTGTACAACCTTCTCTGCCAAGGTTATGGCTGACCAGCTCCGCAAG
CCTCCCAGCCGAGACCAGTGGAGCATGACCCCCAGACAGTGAATGCCTACTACCTTCCAATAAGAATGAGATC
GTCTTCCCCGCTGGCATCCTGCAGGCCCTTCTATGCCCGCAACACCCCAAGGCCCTGAACTTCGGTGGCATC
GGTGTGGTCATGGGCCATGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTG
CGGCCCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACACACGGCCTGCATGGAGGAACAGTACAATCAA
TACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACATTACTGACAACGGGGGGCTGAAG
GCTGCCACAAATGCTTACAAAGCATGGCTGAGAAAGCATGGGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACC
AACCACCAGCTCTTCTTCGTGGGATTTGCCAGGTGTGGTGCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGG
CTGGTGACCGACCCCAACAGCCCTGCCCGCTTCCGCGTGTGGGCACTCTCTCCAACCTCCCGTGACTTCTTCCGG
CACTTCGGCTGCCCTGTGGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACCTGGATCAGGGGA
GAAATGGCCAGCTGTCAACAGACCTGGGGCAGCTCTCTGACAAAGCTGTTTGCTCTTGGGTTGGGAGGAAGCAA
ATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCCACAGGTGACATGAGTACAGACCCTCCTCAATCACCACATTG
TGCCTCTGCTTTGGGGGTGCCCTGCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTCCGTGTACCCT
GCCTGGAAGAGGTCTGGGTGGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCC

FIGURE 225

MNVALQELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSH
STCLTEACIRVAGKILESIDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQA
ILKHLLENTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLEKIGGWNITGPWDQDN
FMEVLKAVAGTYRATPFFTUYISADSKSSNSNVIQVDQSGFLPSRDYYLNRTANEKVLTA
LDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRRDEEKIYHKMSISELQALAP
SMDWLEFLSFLLSPLELSDSEPVVVYGMDYLQQVSELINRTEPSILNNYLIWNLVQKTTSSL
DRRFESAQEKLLLETLYGTTKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKEIAEGMI
SEIRTAFFEEALGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISEDSF
FQNMLNLYNFSKVMADQLRKPPSRDQWSMTPQTVNAYYLPKNEIVFPAGILQAPFYARNH
PKALNFGGIGVVMGHELTHAFDDQGREYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQYQV
NGERLNGRQTLGENITDNGGLKAAYNAYKAWLRKHGEEQQLPVGLTNHQLFFVGFAQVWCS
VRTPESSHEGLVTDPHSPARFRVLGTLSNSRDFLRHFGCPVGSPMNPGLCEVW

Type II Transmembrane domain:

amino acids 32-57

FIGURE 226

GCCCCGGCCCTCCGCCCTCCGCACTCCCGCCTCCCTCCCTCCGCCCGCTCCCGCGCCCTCCTCCCTCCCTCCTCCC
 CAGCTGTCCCGTTCGCGTCATGCCGAGCCTCCCGGCCCGCGGCCCGCTGCTGCTCCTCGGGCTGCTGCTGCT
 CGGCTCCCGGCCCGGCCCGCGGCCCGAGACCCCGCTGCTGCCCATCCGTTCTGAGAAGGAGCCGCTGCC
 CGTTCGGGGAGCGGCAGGTAGGTGGGCGCCCGGGGGAGGCGCGGGCGGGGAGTCCGGCTCGGGGCGAGTCAGCGC
 CAGCCCGGAGGGGGCGCGGGGCGCAGGTGGCTCGGCGCGGCGGGCGGCCCGGAGGGTGGGCGGGGGCAGAAGGGC
 GCGGTGCCTGGGACCCGGGACCCGCGGGCAGCCCCCGGGGCGGCACACGGCGCGAGCTGGGCAGCGGCCTCCAGC
 CAAGCCCGTCCCCGAGGCTGCACCTTCGCGCGGAAGTCTATGCCTTGGACGAGACGTGGCACCCCGGACCTAGG
 GGAGCCATTCCGGGTGATGCGCTGCGTGCTGTGCGCCTGCGAGGCGCAGTGGGGTCCCGTACCAGGGGCCCTGG
 CAGGGTCAGTGCAGAACATCAAACACAGAGTGCCCAACCCCGGCCTGTGGGCAGCCCGCCAGCTGCCGGGACA
 CTGCTGCCAGACCTGCCCCAGGACTTCGTGCGCTGCTGACAGGGCCGAGGTGCGAGGCGGTGGCACGAGCCCG
 AGTCTCGCTGCTGCGCTCTAGCCTCCGCTTCTCTATCTCCTACAGGCGGCTGGACCGCCCTACCAGGATCCGCTT
 CTCAGACTCCAATGGCAGTGTCTGTTTGAACACCTGCAGCCCCACCAAGATGGCCTGGTCTGTGGGGTGTG
 GCGGGCAGTGCCTCGGTTGTCTCTGCGCTCCTTAGGGCAGAACAGCTGCATGTGGCACTTGTGACACTCACTCA
 CCCTTCAGGGGAGGTCTGGGGGCTCTCATCCGGCACCGGGCCCTGTCCCCAGAGACCTTCAGTGCCATCCTGAC
 CCTAGAAGGCCCCCAGCAGGGCGTAGGGGGCATCACCTGCTCACTCTCAGTGACACAGAGGACTCCTTGCA
 TTTTTTGCTGCTCTTCCGAGGCCTTGACAGGACTAACCCAGGTTCCCTTGAGGCTCCAGATTCTACACAGGGGCA
 GCTACTGCGAGAATTTCAGGCCAATGTCTCAGCCAGGAACAGGCTTTGCTGAGGTGCTGCCCAACCTGACAGT
 CCAGGAGATGGACTGGCTGGTGTGCTGGGGGAGCTGCAGATGGCCCTGGAGTGGGCAGGCAGGCCAGGGCTGCGCAT
 CAGTGGACACATTGCTGCCAGGAAGAGCTGCGACGTCCTGCAAAGTGTCTTTGTGGGGCTAATGCCCTGATCCC
 AGTCCAAACGGGTGCTGCCGGCTCAGCCAGCCTCACTCTGCTAGGAAATGGCNCCTGATCCTCCAGGTGCAATT
 GGTAGGGACAACCAAGTGGTGGTGGCCATGACACTGGAAACCAAGCCTCAGCGGAGGGATCAGCCCACTGTCTCT
 GTGCCACATGGCTGGCCTATCCTCCCCGCGCCCGGCGGTGGGTATCTGCCCTGGGCTGGGGTGCCGAGGGGC
 TCATATGCTGCTGCAGAATGAGCTCTTCTGAACGTGGGCACCAAGGACTTCCAGACGGAGAGCTTCGGGGGCA
 ACGTGGCTGCCCTGCCCTACTGTGGGGCATAGCGCCCGCCCTGCCCGTGGCCCTAGCAGGAGCCCTGGTGTACC
 CCCTGTGAAGAGCCAAGCAGCAGGGCACGCTGGCTTTCTTGGATACCCACTGTCACTGCACTATGAAGTGTCT
 GCTGGCTGGGCTTGGTGGCTCAGAACAGGCACTGTCACTGCCCACCTCCTTGGGCTCCTGGAACGCCAGGGCC
 TCGGCGGCTGCTGAAGGATTTCTATGGCTCAGAGGCCAGGGTGTGGTGAAGGACCTGGAGCCGGAACCTGCTGCG
 GCACCTGGCAAAGGCATGGCTTCCCTGATGATCACCAACCAAGGTAGCCCCAGAGGGGAGCTCCGAGGGCAGCCT
 CTCTCCAGGTGCACATAGCCAACCAATGTGAGGTTGGCGGACTGCGCCTGGAGGCGGCCGGGGCCGAGGGGGT
 GCGGGCGCTGGGGGCTCCGGATACAGCCTCTGCTGCGCCGCTGTGGTGCCTGGTCTCCCGGCCCTAGCGCCCGC
 CAAACCTGGTGGTCTTGGGCGGCCCGGAGACCCCAACACATGCTTCTTGGAGGGGAGCAGCGCCCCACGGGGC
 TCGCTGGGCGCCCAACTACGACCCGCTCTGCTCACTGCACTGCGCAGAGACGAACGGTGATCTGTGACCCGGT
 GGTGTGCCCAACCGCCAGCTGCCACACCCGGTGACGCTCCCGACCAAGTGTGCTGCCCTGTTTGGCTTGGCTGCTA
 TTTTGATGGTGACCGGAGCTGGCGGGCAGCGGGTACGCGTGGCACCCCGTTGTGCCCCCTTTGGCTTAATTA
 GTGTGCTGTCTGCACCTGCAAGCAGGGGGGCACTGGAGAGGTGCACTGTGAGAAGGTGCACTGTCCCCGGCTGGC
 CTGTGCCAGCCTGTGCGTGTCAACCCACCGACTGCTGCAAACAGTGTCCAGGTGAGGCCCCACCCAGCTGGG
 GGACCCCATGCAGGCTGATGGGCCCCGGGGCTGCCGTTTGTGCTGGGCACTGGTTCAGAGAGTCAAGCTGGCA
 CCCCTCAGTGCCCCCGTTTGGAGAGATGAGCTGTATCACTGCAGATGTGGGGTAAGTGGGGAGCAGAGGCTTGT
 CTGAGGTGGGTACTGGGAGCCTGGTCTGGAGTAGGAGACTTCCAGGGAGGTCCCTGAAGAAGCTGAAGGTCA
 CTGTGTCCAGTGCCTCTGGGGGACACTCAGTGTCTGCTCTGTCTTGTACCAGGACGGGGTGCCTCACTGTGAGC
 GGGATGACTGTTCACTGCCACTGTCTGTGGCTCGGGGAAGGAGAGTCGATGCTGTTCCCGCTGCACGGCCACC
 GCGCGCGTAAGTGAGGGAGTCCAGGGTCAGCAGCTGTGAGTGGAGGGCTCACCTGCCTGTGGGACTCCTGATCAG
 GGAAGGGAGCACTCACTGTGTGCAGGAACAGTGCAGCCTGCCTCACAAGTGCCATTCCAATCCACCTCACAGCA
 ACCTGGTGGAAATTGTTATTTATGACCTTTTCTTTACAAATGAGATTTCTGAAGCTCAGAGAAATTAAGCAACGAG
 ATGAAGGTCAACCAGCTGTGTGCACTGACCTGTTTAGAAAATACTGGCCTTTCTGGGACCAAGGCAGGGATGCTT
 TGCCCTGCCCTCTATGCCTCTCTGTGCTCTCCACTCCCTCTCCCCCTCTCCAACATTCCCTCCCTTCTGTCTCC
 AGCAGCCCCAGAGACCAGAACTGATCCAGAGCTGGAGAAAGAAGCCGAAGGCTCTTAGGGAGCAGCCAGAGGGCC
 AAGTGACCAAGAGGATGGGGCCTGAGCTGGGGAAGGGGTGGCATCGAGGACCTTCTTGCACTTCTCTGTGGGAAG
 CCCAGTGCCCTTGTCTCTGTCTCTGCTCTACTCCACCCCACTACCTCTGGGAACCAAGCTCCACAAGGGG
 GAGAGGCAGCTGGGCCAGACCGAGGTACAGCCACTCAAGTCTGCCCCTGCCACCCTCGGCCTCTGTCTGGAA
 GCCCCACCCCTTTCTTCTGTACATAATGTCACTGGCTTGTGGGATTTTAAATTTATCTTCACTCAGCACCAG
 GGCCCCGACACTCCACTCCTGCTGCCCCCTGAGCTGAGCAGAGTCAATTTATGGAGAGTTTGTATTTATTAAG
 ATTTCTTTTTTCACTCTTTGGGCATGAGGTTGGCTCTTTGTGGCCAGGAACCTGAGTGGGGCCTGGTGGAGAAGGG
 GCNGAGAGTAGGAGGTGAGAGAGAGGAGCTCTGACACTTGGGGAGCTGAAAGAGACCTGGAGAGGCAGAGGATAG
 CGTGGCANNITGGCTGGCATNCTGGGTTCCGAGAGGGGCTGGGGATGGTCTTGTGAGATGGTCTAGAGACTCAAG
 AATTTAGGGAAGTAGAAGCAGGATTTTGACTCAAGTTTAGTTTCCACATCGCTGGCCTGTTTGTGACTTCATG
 TTTGAAGTTGCTCCAGAGAGAGAATCAAAGGTGTCAACAGCCCTCTCTCCCTCCTTCCCTTCCCTTCTTCT
 TTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC

FIGURE 227

GGCCGAGCGGGGGTGCTGCGCGGCGGCCGTGATGGCTGGTGACGGCGGGGCCGGGCAGGGGA
CCGGGGCCGCGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGAATCACCGCCTGGCCCCGAC
TCCACCATGAACGTGCGGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAGAAGGG
GACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTAC
TGCTGGCTGCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCA
TCCCACAGCACCTGCCTTACAGAGGCCTGCATTTCGAGTGGCTGGAAAAATCCTGGAGTCCCT
GGACCGAGGGGGTGAGCCCCCTGTGAGGACTTTTACCAGTTCTCCTGTGGGGGCTGGATTTCGGA
GGAACCCCTGCCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGCCTCTGGGACCAAAC
CAGGCCATACTGAAGCACCTGCTTGAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAGCA
GAAGACACAGCGCTTCTACCTATCTTGCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCC
AGCCACTGAGAGACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAG
GACAACTTTATGGAGGTGTTGAAGGCAGTAGCAGGGACCTACAGGGCCACCCCATTTCTTCAC
CGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGCAATGTTATCCAGGTGGACCAGTCTG
GGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAGAAAGTAAGGAAC
ATCTTCCGAACCCCCATCCCTACCCCTGGCTGAGCTGGGCTGATCCCTGTTGACTTTTCCCT
TTGCCAAGGGTCAGAGCAGGGAAGGTGAGCCTATCCTGTCACCTAGTGAACAACTGCCCCCT
CCTTTCTTTCTTCTTTTCTTCCCTCCCTCCCTTTCTTCCCCTTTTCCTTCCTTCCTTCC
TCTTATTCTTCTAGTAGGTTTCATAGACACCTACTGTGTGCCAGGTCCAGTGGGGGAATTCG
GAGATATAAGTTTCCGAGCCATTGCCACAGGAAGCGTTCAGTGTGATGGGTTTCATGGACCT
AGATAGGCTGATAACAAAGCTCACAAGAGGGTCCTGAGGATTCAGGAGAGACTTATGGAGCC
AGCAAAGTCTTCCTGAAGAGATTGCATTTGAGCCAGGTCTCTGTAG

FIGURE 228

ATGCCTACTACCTTCCAAC TAAGAATGAGATCGTCTTCCCCGCTGGCATCCTGCAGGCCCCC
TTCTATGCCCCGAACCAACCCCAAGGCCCTGAACTTCGGTGGCATCGGTGTGGTCATGGGCCA
TGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTGCGGC
CCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACCAACACGGCCTGCATGGAGGAACAG
TACAATCAATACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACAT
TGCTGACAACGGGGGGCTGAAGGCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATG
GGGAGGAGCAGCAACTGCCAGCCGTGGGGCTACCAACCACCAGCTCTTCTTCGTGGGATTT
GCCCAGGTGTGGTGCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGGGCTGGTGACCGACCC
CCACAGCCCTGCCCCGCTTCCGCGTGCTGGGCACCTCTCTCAACTCCCGTGACTTCCTGCGGC
ACTTCGGCTGCCCTGTGCGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACC
TGGATCAGGGGAGAAATGGCCAGCTGTCACCAGACCTGGGGCAGCTCTCCTGACAAAGCTGT
TTGCTCTTGGGTGGGAGGAAGCAAATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCCACA
GGTGACATGAGTACAGACCCTCCTCAATCACCACATTGTGCCTCTGCTTTGGGGGTGCCCTT
GCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTTCCGTGTCACCCTGCCTGGAAGAG
GTCTGGGTGGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCCTCTTCTGTCCCCAGGCTCACT
CAGCCTGGCGGCCATGGGGCCTGCCGTGCCTGCCCCACTGTGACCCACAGGCCTGGGTGGTG
TACCTCCTGGACTTCTCCCCAGGCTCACTCAGTGCGCACTTAGGGGTGGACTCAGCTCTGTC
TGGCTCACCTCACGGGCTACCCCCACCTCACCTGTGCTCCTTGTGCCACTGCTCCCAGTG
CTGCTGCTGACCTTCACTGACAGCTCCTAGTGGAAGCCCAAGGGCCTCTGAAAGCCTCCTGC
TGCCCACTGTTTCCCTGGGCTGAGAGGGGAAGTGCATATGTGTAGCGGGTACTGGTTCCTGT
GTCTTAGGGCACAAAGCCTTAGCAAATGATTGATTCTCCCTGGACAAAGCAGGAAAGCAGATA
GAGCAGGGAAAAGGAAGAACAGAGTTTATTTTACAGAAAAGAGGGTGGGAGGGTGTGGTCT
TGGCCCTTATAGGACC

FIGURE 229

CCCACGCGTCCGAGCCGCCCGAGAATTAGACACACTCCGGACGCGGCCAAAAGCAACCGAGA
GGAGGGGAGGCCAAAAACACCGAAAAACAAAAGAGAGAAACAACACCCAACAACCTGGGGTGG
GGGGAAGAAAGAAAGAAAAAGAAACCCACCCACCCACCAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAATCCTGTGGCGCGCCGCTGGTTCCCGGGAAGACTCGCCAGCACCAGGGGG
TGGGGGAGTGCAGAGCTGAAAGCTGCTGGAGAGTGAAGCAGCCCTAGCAGGGATGGACATGATG
CTGTTGGTGCAGGGTGTCTTGTGCTCGAACCAGTGGCTGGCGGCGGTGCTCCTCAGCCTGTG
CTGCCTGCTACCCTCCTGCCTCCCGGCTGGACAGAGTGTGGACTTCCCTGGGCGGCCGTGG
ACAACATGATGGTCAGAAAAGGGGACACGGCGGTGCTTAGGTGTTATTTGGAAGATGGAGCT
TCAAAGGGTGCCTGGCTGAACCGGTCAAGTATTATTTTTGCGGGAGGTGATAAGTGGTCAGT
GGATCCTCGAGTTTCAATTTCAACATTGAATAAAAGGGACTACAGCCTCCAGATACAGAATG
TAGATGTGACAGATGATGGCCCATACACGTGTTCTGTTTCACTCAACATACACCCAGAACA
ATGCAGGTGCATCTAACTGTGCAAGTTCCTCCTAAGATATATGACATCTCAAATGATATGAC
CGTCAATGAAGGAACCAACGTCACTCTTACTTGTGTTGGCCACTGGGAAACCAGAGCCTTCCA
TTTCTTGGCGACACATCTCCCATCAGCAAAACCATTTGAAAATGGACAATATTTGGACATT
TATGGAATTACAAGGGACCAGGCTGGGGAATATGAATGCAGTGCAGGAAAATGCTGTGTCATT
CCCAGATGTGAGGAAAGTAAAAGTTGTTGTCAACTTTGCTCCTACTATTAGGAAATTAAAT
CTGGCACCGTGACCCCGGACGCAGTGGCCTGATAAGATGTGAAGGTGCAGGTGTGCCGCT
CCAGCCTTTGAATGGTACAAAGGAGAGAAGAAGCTCTTCAATGGCCAACAAGGAATTATTAT
TCAAATTTTAGCACAAAGATCCATTCTCACTGTTACCAACGTGACACAGGAGCACTTCGGCA
ATTATACCTGTGTGGCTGCCAACAAGCTAGGCACAACCAATGCGAGCCTGCCTCTTAACCT
CCAAGTACAGCCAGTATGGAATTACCGGGAGCGCTGATGTTCTTTTCTCCTGCTGGTACCT
TGTGTTGACACTGTCTCTTTACCAGCATATTCTACCTGAAGAATGCCATTCTACAATAAA
TTCAAAGACCCATAAAAGGCTTTTAAGGATTCTCTGAAAGTGCTGATGGCTGGATCCAATCT
GGTACAGTTTGTAAAGCAGCGTGGGATATAATCAGCAGTGCTTACATGGGGATGATCGCC
TTCTGTAGAATTGCTCATTATGTAAATACTTTAATTCTACTCTTTTTTTGATTAGCTACATTA
CCTTGTGAAGCAGTACACATTGTCTTTTTTTAAGACGTGAAAGCTCTGAAATTACTTTTAG
AGGATATTAATTGTGATTTTATGTTTGTAAATCTACAACTTTTCAAAGCATTTCAGTCATGGT
CTGCTAGGTTGCAGGCTGTAGTTTACAAAACGAATATTGCAGTGAATATGTGATTCTTTAA
GGCTGCAATACAAGCATTTCAGTTCCCTGTTTCAATAAGAGTCAATCCACATTTACAAAGATG
CATTTTTTTCTTTTTTTGATAAAAAAGCAAATAATATTGCCTTCAGATTATTTCTTCAAATA
TAACACATATCTAGATTTTTCTGCTTGCATGATATTTCAGGTTTCAGGAATGAGCCTTGTAAT
ATAACTGGCTGTGCAGCTCTGCTTCTCTTTCCTGTAAGTTTCAGCATGGGTGTGCCTTCATAC
AATAATATTTTTCTCTTTGTCTCCAATAATATAAAATGTTTTGCTAAATCTTACAATTTGA
AAGTAAAAATAAACAGAGTGATCAAGTTAAACCATACACTATCTCTAAGTAACGAAGGAGC
TATTGGACTGTAAAAATCTCTTCTGCACTGACAATGGGGTTTGAGAATTTTGCCCCACACT
AACTCAGTTCTTGTGATGAGAGACAATTTAATAACAGTATAGTAAATATACCATATGATTTT
TTTAGTTGTAGCTAAATGTTAGATCCACCGTGGGAAATCATTCCCTTTAAATGACAGCACA
GTCCACTCAAAGGATTGCCTAGCAATACAGCATCTTTTCTTTTCACTAGTCCAAGCCAAAA
TTTTAAGATGATTTGTGAGAAAGGGCACAAAGTCCTATCACCTAATATTACAAGAGTTGGTA
AGCGCTCATCATTAATTTTATTTTGTGGCAGGTATTATGACAGTCGACCTGGAGGGTATGGA
TATGGATATGGACGTTCCAGAGACTATAATGGCAGAAACCAGGGTGGTTATGACCGCTACTC
AGGAGGAAATTACAGAGACAATTATGACAACCTGAAATGAGACATGCACATAATATAGATACA
CAAGGAATAATTTCTGATCCAGGATCGTCCTTCAAATGGCTGTATTTATAAAGGTTTTTGG
AGCTGCACTGAAGCATCTTATTTTATAGTATATCAACCTTTTGTTTTTTAAATTTTCTGCCTATTTAA
AGGATAGCTGAAGACCTTTTAGACAGTTCCATCTTTTTTTTTTAAATTTTTTCTGCCTATTTAA
AGACAAATTATGGGACGTTTGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 230

MMLLVQGACCSNQWLA AVL LLSLCCLLPSCLPAGQSVDFPWA AVDNMMVRKGD TAVLR CYLED
GASKGAWLNRSSII FAGGDKWSVDPRVSISTLNKRDYSLQIQNV DVTDDGPYTCSVQTQHTP
RTMQVHLTVQVPPKIIDISNDMTVNEGTVNLTCLATGKPEPSISWRHISPSAKPFENGQYL
DIYGITRDQAGEYECSAENAVSFPDVRKVKVVVNFAPTIQEIKSGTVTPGRSGLIRCEGAGV
PPPAFEWYKGEKKLFNGQQGII IQNFSTRSILTVTNVTQEHFGNYTCVAANKLGTTNASLPL
NPPSTAQYGITGSADVLFSCWYLVLTLSSTSI FYLKNA ILQ

Important features of the protein:

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 326-345

N-glycosylation sites.

amino acids 71-75, 153-157, 273-277, 284-288, 292-296, 305-309

Casein kinase II phosphorylation site.

amino acids 147-151, 208-212, 224-228

Tyrosine kinase phosphorylation site.

amino acids 178-186

N-myristoylation sites.

amino acids 7-13, 63-70, 67-73, 151-157, 239-245, 291-297,
302-308, 319-325

Myelin P0 protein:

amino acids 92-121

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TOSTOT 187660

FIGURE 231

AGTGGTTCGATGGGAAGGATCTTTCTCCAAGTGGTTCCTCTTGAGGGGAGCATTCTGCTGG
CTCCAGGACTTTGGCCATCTATAAAGCTTGGCAATGAGAAATAAGAAAATTCTCAAGGAGGA
CGAGCTCTTGAGTGAGACCCAACAAGCTGCTTTTACCAAATTGCAATGGAGCCTTTCGAAA
TCAATGTTCCAAAGCCCAAGAGGAGAAATGGGGTGAACCTCTCCCTAGCTGTGGTGGTCATC
TACCTGATCCTGCTCACCGCTGGCGCTGGGCTGCTGGTGGTCCAAGTTCTGAATCTGCAGGC
GCGGCTCCGGGTCTTGAGATGTATTTCTCAATGACACTCTGGCGGCTGAGGACAGCCCGT
CCTTCTCCTTGCTGCAGTCAGCACACCCTGGAGAACACCTGGCTCAGGGTGCATCGAGGCTG
CAAGTCCTGCAGGCCCAACTCACCTGGGTCCGCGTCAGCCATGAGCACTTGCTGCAGCGGGT
AGACAACTTCACTCAGAACCAGGGATGTTTCAAGATCAAAGGTGAACAAGGCGCCCCAGGTC
TTCAAGGTCACAAGGGGGCCATGGGCATGCCTGGTGCCCCCTGGCCCGCCGGGACCACCTGCT
GAGAAGGGAGCCAAGGGGGCTATGGGACGAGATGGAGCAACAGGCCCCCTCGGGACCCCAAGG
CCCACCGGGAGTCAAGGGAGAGGCGGGCCTCCAAGGACCCCAGGGTGCTCCAGGGAAGCAAG
GAGCCACTGGCACCCCAGGACCCCAAGGAGAGAAGGGCAGCAAAGGCGATGGGGGTCTCATT
GGCCCAAAGGGGAACTGGAACCTAAGGGAGAGAAAGGAGACCTGGGTCTCCAGGAAGCAA
AGGGGACAGGGGCATGAAAGGAGATGCAGGGGTCTGAGGGCCTCCTGGAGCCAGGGGAGTA
AAGGTGACTTCGGGAGGCCAGGCCCACCAGGTTTGGCTGGTTTTCTTGAGCTAAAGGAGAT
CAAGGACAACCTGGACTGCAGGGTGTTCCGGGCCCTCCTGGTGCAGTGGGACACCCAGGTGC
CAAGGGTGAGCCTGGCAGTGCTGGCTCCCCTGGGCGAGCAGGACTTCCAGGGAGCCCCGGGA
GTCCAGGAGCCACAGGCCTGAAAGGAAGCAAAGGGGACACAGGACTTCAAGGACAGCAAGGA
AGAAAAGGAGAATCAGGAGTTCAGGCCCTGCAGGTGTGAAGGGAGAACAGGGGAGCCCAGG
GCTGGCAGGTCCCAAGGGAGCCCCTGGACAAGCTGGCCAGAAGGGAGACCAGGGAGTGAAAG
GATCTTCTGGGGAGCAAGGAGTAAAGGGAGAAAAAGGTGAAAGAGGTGAAAACCTCAGTGTCC
GTCAGGATTGTCGGCAGTAGTAACCGAGGCCGGGCTGAAGTTTACTACAGTGGTACCTGGGG
GACAATTTGCGATGACGAGTGGCAAAATTCTGATGCCATTGTCTTCTGCCGCATGCTGGGTT
ACTCCAAAGGAAGGGCCCTGTACAAAGTGGGAGCTGGCACTGGGCAGATCTGGCTGGATAAT
GTTCAGTGTCGGGGCACGGAGAGTACCCTGTGGAGCTGCACCAAGAATAGCTGGGGCCATCA
TGACTGCAGCCACGAGGAGGACGCAGGCGTGGAGTGCAGCGTCTGACCCGAAACCCTTTCA
CTTCTCTGCTCCCGAGGTGTCCTCGGGCTCATATGTGGGAAGGCAGAGGATCTCTGAGGAGT
TCCCTGGGGACAACTGAGCAGCCTCTGGAGAGGGGCCATTAATAAAGCTCAACATCATTGA

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FIGURE 232

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA68886

><subunit 1 of 1, 520 aa, 1 stop

><MW: 52658, pI: 9.16, NX(S/T): 3

MRNKKILKEDELLSETQQAAFHQIAMEPFEINVPKPKRRNGVNFSLAVVVIYLILLTAGAGL
LVVQVLNLQARLRVLEMYFLNDTLAAEDSPSFSLLQSAHPGEHLAQGASRLQVLQAQLTWVR
VSHEHLLQRVDNFTQNPGMFRIKGEQGAPGLQGHKGAMGMPGAPGPPGPPAEKGAKGAMGRD
GATGPSGPQGPPGVKGEAGLQGPQGAPGKQGATGTPGPQGEKSGKGDGGLIGPKGETGTKGE
KGDGLPGSKGDRGMKGDAVMGPPGAQGSKGDFGRPGPPGLAGFPAGKGDQGPGLQGVPG
PPGAVGHPGAKGEPGSAGSPGRAGLPGSPGSPGATGLKSGKGDGTGLQGGQGRKGESGVP
GPA
GVKGEQGSPLAGPKGAPGQAGQKGDQGVKGSSEQGVKGEKGERGENSVSVRIVGSSNRGR
AEVYYSGTWGTICDDEWQNSDAIVFCRMLGYSKGRALYKVGAGTGQIWLNDNVQCRGTESTLW
SCTKNSWGHHDSCSHEEDAGVECSV

Transmembrane domain:

amino acids 47-66 (type II)

N-glycosylation sites.

amino acids 43-47, 83-87, 136-140

Tyrosine kinase phosphorylation site.

amino acids 432-440

N-myristoylation sites.

amino acids 41-47, 178-184, 253-259, 274-280, 340-346, 346-352,
400-406, 441-447, 475-481, 490-496, 515-521

Amidation site.

amino acids 360-364

Leucine zipper pattern.

amino acids 56-78

Speract receptor repeat

amino acids 422-471, 488-519

Clq domain proteins.

amino acids 151-184, 301-334, 316-349

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FIGURE 233

CCCACGCGTCCGAAGGCAGACAAAGGTTCAATTTGTAAAGAAGCTCCTTCCAGCACCTCCTCT
CTTCTCCTTTTGCCCAAACCTACCCAGTGAGTGTGAGCATTTAAGAAGCATCCTCTGCCAAG
ACCAAAAGGAAAGAAGAAAAAGGGCCAAAAGCCAAAATGAAACTGATGGTACTTGTTTTTAC
CATTGGGCTAACTTTGCTGCTAGGAGTTCAAGCCATGCCTGCAAATCGCCTCTCTTGCTACA
GAAAGATACTAAAAGATCACAACCTTCCGGAAGGAGTAGCTGACCTGACACAG
ATTGATGTCAATGTCCAGGATCATTTCTGGGATGGGAAGGGATGTGAGATGATCTGTTACTG
CAACTTCAGCGAATTGCTCTGCTGCCCAAAGACGTTTTCTTTGGACCAAAGATCTCTTTTCG
TGATTCCTTGCAACAATCAATGAGAATCTTCATGTATTCTGGAGAACACCATTCTGATTTTC
CCACAACTGCACTACATCAGTATAACTGCATTTCTAGTTTCTATATAGTGCAATAGAGCAT
AGATTCTATAAATTCTTACTTGTCTAAGACAAGTAAATCTGTGTTAAACAAGTAGTAATAAA
AGTTAATTCAATCTAAAAAAAAAAAAAA

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FIGURE 234

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52758

<subunit 1 of 1, 98 aa, 1 stop

<MW: 11081, pI: 6.68, NX(S/T): 1

MKLMVLVFTIGLTLLLG VQAMPANRLSCYRKILKDHNCHNLPEGVADLTQIDVNVQDHFWDG

KGCEMICYCNFSELLCCPKDVFFGPKISFVIPCNNQ

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 72-76

Tyrosine kinase phosphorylation site.

amino acids 63-71

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TOSTOT-18782660

FIGURE 235

CCCACGCGTCCGCGGACGCGTGGGCTGGACCCAGGTCTGGAGCGAATTCAGCCTGCAGGG
CTGATAAGCGAGGCATTAGTGAGATTGAGAGAGACTTTACCCCGCCGTGGTGGTTGGAGGGC
GCGCAGTAGAGCAGCAGCACAGGCGCGGGTCCCGGGAGGCCGGCTCTGCTCGCGCCGAGATG
TGGAATCTCCTTCACGAAACCGACTCGGCTGTGGCCACCGCGCGCCGCCGCGCTGGCTGTG
CGCTGGGGCGCTGGTGTGGCGGGTGGCTTCTTTCTCCTCGGCTTCCTCTTCGGGTGGTTTA
TAAAATCCTCCAATGAAGCTACTAACATTACTCCAAAGCATAATATGAAAGCATTTTTGGAT
GAATTGAAAGCTGAGAACATCAAGAAGTTCTTACATAATTTTACACAGATAACCACATTTAGC
AGGAACAGAACAAAACCTTTCAGCTTGCAAAGCAAATTCAATCCCAGTGGAAGAATTTGGCC
TGGATTCTGTTGAGCTAGCTCATTATGATGTCTGTGTCTACCCAAATAAGACTCATCCC
AACTACATCTCAATAATTAATGAAGATGGAATGAGATTTTCAACACATCATTATTTGAACC
ACCTCCTCCAGGATATGAAAATGTTTCGGATATTGTACCACCTTTCAGTGCTTCTCTCCTC
AAGGAATGCCAGAGGGCGATCTAGTGTATGTTAACTATGCACGAACTGAAGACTTCTTTAAA
TTGGAACGGGACATGAAAATCAATTGCTCTGGGAAAATTGTAATTGCCAGATATGGGAAAGT
TTTCAGAGGAAATAAGGTTAAAAATGCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTACT
CCGACCCTGCTGACTACTTTGCTCCTGGGGTGAAGTCTATCCAGACGGTTGGAATCTTCCT
GGAGGTGGTGTCCAGCGTGGAATATCCTAAATCTGAATGGTGCAGGAGACCCTCTCACACC
AGGTTACCCAGCAAATGAATATGCTTATAGGCGTGGAATTGCAGAGGCTGTTGGTCTTCCAA
GTATTCCTGTTTCATCCAATTGGATACTATGATGCACAGAAGCTCCTAGAAAAAATGGGTGGC
TCAGCACCACCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGG
CTTTACTGGAACTTTTCTACACAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGA
CGAGAATTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAGACAGATATGTCATT
CTGGGAGGTCACCGGGACTCATGGGTGTTTGGTGGTATTGACCCTCAGAGTGGAGCAGCTGT
TGTTTCATGAAATTGTGAGGAGCTTTGGAACACTGAAAAAGGAAGGGTGGAGACCTAGAAGAA
CAATTTTGTGTTGCAAGCTGGGATGCAGAAGAATTTGGTCTTCTTGGTTCTACTGAGTGGGCA
GAGGAGAATTCAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTGACTCATCTAT
AGAAGGAACTACACTCTGAGAGTTGATTGTACACCGCTGATGTACAGCTTGGTACACAACC
TAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAATCTCTTTATGAAAGTTGG
ACTAAAAAAGTCTTCCCCAGAGTTCAGTGGCATGCCCAGGATAAGCAAATTGGGATCTGG
AAATGATTTTGAAGGTGTTCTTCCAACGACTTGGAATTGCTTCAGGCAGAGCACGGTATACTA
AAAATTGGGAAACAAACAAATTCAGCGGCTATCCACTGTATCACAGTGTCTATGAAACATAT
GAGTTGGTGGAAAAGTTTTATGATCCAATGTTTAAATATCACCTCACTGTGGCCCAGGTTTCG
AGGAGGGATGGTGTGTTGAGCTAGCCAATTCATAGTGCTCCCTTTTGATTGTGAGATTATG
CTGTAGTTTTAAGAAAGTATGCTGACAAAATCTACAGTATTTCTATGAAACATCCACAGGAA
ATGAAGACATACAGTGTATCATTTGATTCACTTTTTTCTGCAGTAAAGAATTTTACAGAAAT
TGCTTCCAAGTTCAGTGAGAGACTCCAGGACTTTGACAAAAGCAACCCAATAGTATTAAGAA
TGATGAATGATCAACTCATGTTTCTGGAAAGAGCATTATTGATCCATTAGGGTTACCAGAC
AGGCCTTTTTTATAGGCATGTCATCTATGCTCCAAGCAGCCACAACAAGTATGCAGGGGAGTC
ATTCCCAGGAATTTATGATGCTCTGTTTGTATTTGAAAGCAAAGTGGACCCTTCCAAGGCCT
GGGGAGAAGTGAAGAGACAGATTTATGTTGCAGCCTTCACAGTGCAGGCAGCTGCAGAGACT
TTGAGTGAAGTAGCCTAAGAGGATTTTTTTAGAGAATCCGTATTGAATTTGTGTGGTATGTCA
CTCAGAAAGAATCGTAATGGGTATATTGATAAATTTTAAAATTGGTATATTTGAAATAAAGT
TGAATATTATATATAA

FIGURE 236

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA52756

><subunit 1 of 1, 750 aa, 1 stop

><MW: 84305, pI: 6.93, NX(S/T): 10

MWNLLHETDSAVATARRPRWLCAGALVLAGGFLLGFLFGWFIKSSNEATNITPKHNMKAFL
DELKAENIKKFLHNFTQIPHLAGTEQNFQLAKQIQSQWKEFGLDSVELAHYDVLVLSYPNKTH
PNYISIINEDGNEIFNTSLFEP PPPGYENVSDIVPPFSAFSPQGMPEGDLVYVNYARTEDFF
KLERDMKINCSGKIVARIYRGKVFRGNKVKNALAGAKGVILYSDPADYFAPGVKSYPDGWNL
PGGGVQQRGNILNLNGAGDPLTPGYPANAYRRGIAEAVGLPSIPVHPIGYDAQKLLEKMG
GSAPPDSSWRGSLKVPYNVPGFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRGAVEPDRYV
ILGGHRDSWVFGGIDPQSGAAVVHEIVRSFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEW
AEENSRLQLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVHNLTKELKSPDEGFEGKSLYES
WTKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWETNKFSGYPLYHSVYET
YELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDYAVVLRKYADKIYSISMKHPQ
EMKTYSVSFDSLFSVAVKNFTEIASKFSERLQDFDKSNPIVLRMMNDQLMFLERAFIDPLGLP
DRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQAAAE
TLSEVA

Signal sequence:

amino acids 1-40

N-glycosylation sites.

amino acids 76-80, 121-125, 140-144, 153-157, 195-199, 336-340,
459-463, 476-480, 638-642

Tyrosine kinase phosphorylation sites.

amino acids 363-372, 605-613, 606-613, 617-626

N-myristoylation sites.

amino acids 85-91, 168-174, 252-258, 256-262, 282-288, 335-341,
360-366, 427-433, 529-535, 707-713